

GenCore version 5.1.7  
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OM nucleic - nucleic search, using sw model

Run on: February 23, 2006, 11:57:54 ; Search time 5416 Seconds  
(without alignments)  
10453.486 Million cell updates/sec

Title: US-10-723-947-75

Perfect score: 996

Sequence: 1 taactgcctctctctctcc.....tagctacttgatgtgtaat 996

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 5893141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.\*

1: gb\_ba.\*  
2: gb\_in.\*  
3: gb\_env.\*  
4: gb\_om.\*  
5: gb\_ov.\*  
6: gb\_pat.\*  
7: gb\_ph.\*  
8: gb\_pt.\*  
9: gb\_ro.\*  
10: gb\_sts.\*  
11: gb\_sy.\*  
12: gb\_un.\*  
13: gb\_vl.\*  
14: gb\_btg.\*  
15: gb\_pl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	848.4	85.2	850	15	AY485965	AY485965 Triticum
2	848.4	85.2	850	15	AY485966	AY485966 Triticum
3	848.4	85.2	850	15	AY485968	AY485968 Triticum
4	846.8	85.0	850	15	AY485967	AY485967 Triticum
5	830.8	83.4	847	15	AY485964	AY485964 Triticum
6	830.8	83.4	850	15	AY485963	AY485963 Triticum
7	776	77.9	792	15	AY485969	AY485969 Triticum
8	561	56.3	110000	15	AY485644_3	Continuation (4 of AY485644_3)
9	464.4	46.6	712	15	AY485975	AY485975 Triticum
10	464.4	46.6	712	15	AY485976	AY485976 Triticum
11	420	42.2	2078	15	AY485979	AY485979 Triticum
12	320.8	32.2	110000	15	AY485644_2	Continuation (3 of AY485644_2)
13	267.2	26.8	1790	15	AY485980	AY485980 Triticum
14	251.4	25.2	2064	15	AY485978	AY485978 Hordeum v
15	247.6	24.9	1985	15	AY485977	AY485977 Hordeum v
16	206.4	20.7	264	15	AY687931	AY687931 Hordeum v
17	157	15.8	687	15	AY485970	AY485970 Triticum
18	157	15.8	687	15	AY485971	AY485971 Triticum

19	152.2	15.3	688	15	AY485972	AY485972 Triticum
20	137.6	13.8	834	15	AY485973	AY485973 Triticum
21	93	9.3	110000	15	AP008213	Continuation (92 o
22	93	9.3	150554	15	AP005307	AP005307 Oryza sat
23	88.2	8.9	944	15	AY082965	AY082965 Hordeum v
24	86	8.6	1258	15	AK109732	AK109732 Oryza sat
25	86	8.6	110000	15	AP008216	Continuation (216
26	86	8.6	144191	15	AC079874	AC079874 Oryza sat
27	86	8.6	300029	15	AE017119	AE017119 Oryza sat
28	79	7.9	1534	15	AY485974	AY485974 Triticum
29	76.6	7.7	885	6	AX050570	AX050570 Sequence
30	76.6	7.7	990	15	BT002107	BT002107 Arabidops
31	76.6	7.7	1103	15	AY140103	AY140103 Arabidops
32	76.6	7.7	1124	15	AY085729	AY085729 Arabidops
33	76.6	7.7	1127	15	AY058130	AY058130 Arabidops
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35	76.6	7.7	103495	15	AC006585	AC006585 Arabidops
36	75.6	7.6	1163	15	AY082960	AY082960 Hordeum v
37	75.6	7.6	1324	15	AY082962	AY082962 Hordeum v
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40	75.4	7.6	170964	15	AP003579	AP003579 Oryza sat
41	74.8	7.5	1396	15	AK121024	AK121024 Oryza sat
42	74.8	7.5	110000	15	AP008210	Continuation (249
43	74.8	7.5	170765	15	OSJN00052	AL606627 Oryza sat
44	74.6	7.5	1386	15	AK100097	AK100097 Oryza sat
45	74.6	7.5	1388	15	AK058536	AK058536 Oryza sat

## ALIGNMENTS

RESULT 1	AY485965	850 bp	mrna	linear	PUN 17-MAR-2004
LOCUS	Triticum monococcum cultivar PI272561 ZCCT1 (VRN2) mRNA, complete cds.				
DEFINITION	AY485965				
ACCESSION	AY485965.1	GI:45390685			
VERSION	Triticum monococcum				
KEYWORDS	Triticum monococcum				
SOURCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Triticum.				
ORGANISM	1 (bases 1 to 850)				
REFERENCE	Yan, L., Loukoianov, A., Blechl, A., Tranquilli, G., Ramakrishna, W., Samiguel, P., Bennettzen, J.L., Echenique, V. and Dubcovsky, J.				
AUTHORS	The Wheat VRN2 Gene Is a Flowering Repressor Down-Regulated by Vernalization				
TITLE	Science 303 (5664), 1640-1644 (2004)				
JOURNAL	15016992				
PUBMED	2 (bases 1 to 850)				
REFERENCE	Yan, L., Loukoianov, A., Blechl, A., Tranquilli, G., Ramakrishna, W., Samiguel, P., Bennettzen, J.L., Echenique, V. and Dubcovsky, J.				
AUTHORS	Submitted (20-NOV-2003) Agronomy and Range Science, University of California, One Shields Avenue, Davis, CA 95616, USA				
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REFERENCE	/mol_type="mRNA"				
AUTHORS	/db_xref="taxon:4568"				
TITLE	/note="winter line"				
JOURNAL	1. .850				
PUBMED	/gene="VRN2"				
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PUBMED	/product="ZCCT1"				
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Best Local Similarity 99.9%; Pred. No. 1.7e-220;
Matches 849; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 74 AAACAAGCAAGCAAACTTGGAGCTAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAG 133
DB 61 AAACAAGCAAGCAAACTTGGAGCTAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAG 120
QY 134 GCGCAACAACTGCGCGGCTCATGTGTCGCCATTCACCATCATCATCATCATCATCATC 193
DB 121 GCGCAACAACTGCGCGGCTCATGTGTCGCCATTCACCATCATCATCATCATCATCATC 180
QY 194 AGGAGCAGCAGCTGTGTGAGTACCACTTCCTCGCCATGGCAACACACACACACAC 253
DB 181 AGGAGCAGCAGCTGTGTGAGTACCACTTCCTCGCCATGGCAACACACACACACAC 240
QY 254 ATGGCTCGGAGCAGACTACCCAGTGCCACCGCGCCAGACAACTTCGACACCGCAGAA 313
DB 241 ATGGCTCGGAGCAGACTACCCAGTGCCACCGCGCCAGACAACTTCGACACCGCAGAA 300
QY 314 CATGACACAGACATTTTATGAAACAGCAGCGCAGGAAACAGCAGCAGGCTCAGCTGG 373
DB 301 CATGACACAGACATTTTATGAAACAGCAGCGCAGGAAACAGCAGCAGGCTCAGCTGG 360
QY 374 AGTGGGCGCAGCGGCGCAACATGGCTTCACTAGTGAGCGCCACCGGAGAGCCCA 433
DB 361 AGTGGGCGCAGCGGCGCAACATGGCTTCACTAGTGAGCGCCACCGGAGAGCCCA 420
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RESULT 2
AY485966
LOCUS
DEFINITION
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ACCESSION
AY485966
VERSION
AY485966.1 GI:45390690
KEYWORDS
Triticum monococcum
SOURCE
Triticum monococcum
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Triticum.
REFERENCE
1 (bases 1 to 850)
Yan, L., Loukianov, A., Blechl, A., Tranquilli, G., Ramakrishna, W.,
SanMiguel, P., Bennett, J. L., Echenique, V. and Dubcovsky, J.,
The Wheat VRN2 Gene Is a Flowering Repressor Down-Regulated by
Vernalization
Science 303 (5664), 1640-1644 (2004)
JOURNAL
PUBMED
15016992
AUTHORS
Yan, L., Loukianov, A., Blechl, A., Tranquilli, G., Ramakrishna, W.,
SanMiguel, P., Bennett, J. L., Echenique, V. and Dubcovsky, J.,
Direct Submission
Submitted (20-NOV-2003) Agronomy and Range Science, University of
California, One Shields Avenue, Davis, CA 95616, USA
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Location/Qualifiers
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ORIGIN
Query Match      85.2%; Score 848.4; DB 15; Length 850;
Best Local Similarity 99.9%; Pred. No. 1.7e-220;
Matches 849; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 14 TTCTTCTCGAGCTCTCTCTCTCTCGGCTCTCCAGCAGCAGACACACAGAAAAAC 73
DB 1 TTCTTCTCGAGCTCTCTCTCTCTCGGCTCTCCAGCAGCAGACACACAGAAAAAC 60
QY 74 AAACAAGCAAGCAAACTTGGAGCTAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAG 133
DB 61 AAACAAGCAAGCAAACTTGGAGCTAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAG 120
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DB 121 GCGCAACAACTGCGCGGCTCATGTGTCGCCATTCACCATCATCATCATCATCATCATC 180
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QY 254 ATGGCTCGGAGCAGACTACCCAGTGCCACCGCGCCAGACAACTTCGACACCGCAGAA 313
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**TITLE**  
JOURNAL  
**FEATURES**

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Qy  61  AAACAACGACGAAACCTTGAGCTAGCTAGCAGTATGTCCTCATGCTCATGGCTTTGTGG 120
Db     |||
Qy  134  GCGCCAAACACTGCCCGCGCTCATGGTCTGCCCATTCACCATTCAACATCATCATCATCATC 193
Db     |||
Qy  121  GGCCACAACTGCCCGGCTCATGCTCTGCCCATTCACCATTCAACATCATCATCATCATC 180
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Qy  194  AGGAGCACCAAGCTGTGTGAGTACCAAGTTCCTTGGCCCATGGCAACCAACCAACCAAC 253
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Qy  181  AGGAGCACCAAGCTGTGTGAGTACCAAGTTCCTTGGCCCATGGCA--ACCAACCAACCAAC 237
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Qy  374  AGGTGGCGCAGCGCGCCAACACATGGCTCACCTAGTGCACCAACCGCGCAAGAGCCCCACA 433
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Qy  358  AGGTGGCGCAGCGCGCCAACACATGGCTCACCTAGTGCACCAACCGCGCAAGAGCCCCACA 417
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Qy  418  TCGTGCCATTTACGAGAGGTGCATTCACAACTATTAGCAATGAAGCAATCATGACTA 477
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Qy  494  TTCACACAGAGATGATGGTGGGGCTGCCCATTTATCCCAATGCAGGAGAGACGACCGA 553
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Db 171 CGCGGACTACCCACGCCACCGCCACCTGCGCCATTCGCCACCACTGCAGATCATGGA 230  
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RESULT 10  
AY485976

LOCUS  
DEFINITION  
Triticum monococcum cultivar P1272561 ZCCT2 (VRN2) mRNA, linear PLN 17-MAR-2004  
cgs.

ACCESSION  
AY485976VERSION  
AY485976.1 GI:45390733KEYWORDS  
Triticum monococcumSOURCE  
Triticum monococcumORGANISM  
Triticum monococcumREFERENCE  
AUTHORS  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Poideae; Triticeae; Triticum.TITLE  
The Wheat VRN2 Gene Is a Flowering Repressor Down-Regulated by  
VernalizationJOURNAL  
Science 303 (5664), 1640-1644 (2004)PUBMED  
15016992AUTHORS  
2 (bases 1 to 712)  
Yan, L., Loukianov, A., Blechl, A., Tranquillini, G., Ramakrishna, W.,  
SanMiguel, P., Bennetzen, J.L., Echenique, V. and Dubcovsky, J.TITLE  
Submitted (20-NOV-2003) Agronomy and Range Science, University of  
California, One Shields Avenue, Davis, CA 95616, USAJOURNAL  
Location/QualifiersFEATURES  
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## ORIGIN

Query Match 46.6%; Score 464.4; DB 15; Length 712;  
Best Local Similarity 81.5%; Pred. No. 1.8e-115;  
Matches 580; Conservative 0; Mismatches 116; Indels 16; Gaps 3;  
QY 80 GCAAGCAAAACCTTGAGCTAGCTAGCTATGTCATGTCATGTCGCGGTTTGTGCGGCGCA 139  
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QY 140 ACAACTGCCCGCTCATGCTCTGCCCATTTCAACATCATCATCATCATCATCATCATCAT 199  
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QY 260 CGGAGCAGACTTACCCAGTCCAGCGCCAGCAACCTTCGACCAACCAACCAACCAACCAAC 319  
Db 171 CGGCGACTACCCAGCGCCAGCGCCAGCGCCAGCGCCAGCGCCAGCGCCAGCGCCAGCG 230  
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QY 380 GCGAGCGCGCCACACATGGCTCACCTAGTGCAGCGCACCGG-----CAAGAGCCACA 433  
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Db 351 TCGTGCCATTTCTCGGGGCTGCATTACCAACACTATTAGCAATGAAGCAATCATGACTA 410  
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QY 554 AGGTGATAGGTATAGGAG 613  
Db 471 AGGTGATAGGTATAGGAG 530  
QY 614 AGTCCAGAAAAGCTTACGCTGAGCTTCGGCGCATGGCTCAACGCGCTTTGTCAAGGTAC 673  
Db 531 AGTCCAGAAAAGCTTACGCTGAGCTTCGGCGCATGGCTCAACGCGCTTTGTCAAGGTAC 590  
QY 674 CCGAAGCCATGGCATGCCCATCATCTCCAGCTTCGCCCTTATGATCCCTAGTAACTTCACC 733  
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Db 651 TCGATGGTTCGGTAAATTTATAGCAACAGCCAGCAATTAATATACATATT 702

## RESULT 11

AY485979

LOCUS

DEFINITION

Triticum turgidum cultivar Langdon ZCCT1-Td (VRN2) gene, complete  
cgs.

ACCESSION

AY485979

VERSION

AY485979.1 GI:45390744

KEYWORDS

AY485979 2078 bp DNA linear PLN 17-MAR-2004  
Triticum turgidum cultivar Langdon ZCCT1-Td (VRN2) gene, complete  
cgs.  
AY485979  
AY485979.1 GI:45390744

SOURCE Triticum turgidum  
ORGANISM Triticum turgidum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Poideae; Triticeae; Triticum.  
REFERENCE 1 (bases 1 to 2078)  
AUTHORS Yan, L., Loukolanov, A., Blechl, A., Tranquilli, G., Ramakrishna, W.,  
SanMiguel, P., Bennett, J. L., Echenique, V. and Dubcovsky, J.  
TITLE The Wheat VRN2 Gene Is a Flowering Repressor Down-Regulated by  
Vernalization  
JOURNAL Science 303 (5664), 1640-1644 (2004)  
PUBMED 15016992  
REFERENCE 2 (bases 1 to 2078)  
AUTHORS Yan, L., Loukolanov, A., Blechl, A., Tranquilli, G., Ramakrishna, W.,  
SanMiguel, P., Bennett, J. L., Echenique, V. and Dubcovsky, J.  
TITLE Direct Submission  
JOURNAL Submitted (20-NOV-2003) Agronomy and Range Science, University of  
California, One Shields Avenue, Davis, CA 95616, USA  
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Query Match 42.2%; Score 420; DB 15; Length 2078;  
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Matches 423; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
QY 436 GTGCCATTTCAGGAGGTGCATTACCAACACTATTAGCAATGAAGCAATCATGACTATT 495  
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QY 496 GACACAGAGATGATGGTGGGGCTGCCCATTTATCCCAATGCAGGAGAGACGCGAAG 555  
DB 1711 GACACAGAGATGATGGTGGGGCTGCCCATTTATCCCAATGCAGGAGAGACGCGAAG 1770  
QY 556 GTGATGAGGTATAGGAG 615  
DB 1771 GTGATGAGGTATAGGAG 1830  
QY 616 TCCAGAAAGCTTACGCTGAGCTTCGGCCATCGGTCACGCGCGCTTTGTCAAGGTACCC 675  
DB 1831 TCCAGAAAGCTTACGCTGAGCTTCGGCCATCGGTCACGCGCGCTTTGTCAAGGTACCC 1890  
QY 676 GAAGCCATGGCATCGCCATCATCTCCAGCTTCGCCCTATGATCCTAGTAAACTTCACCTC 735  
DB 1891 GAAGCCATGGCTCGCCATCATCTCCAGCTTCGCCCTATGATCCTAGTAAACTTCACCTC 1950  
QY 736 GGATGGTTCGGTAATTTATAGCAACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 795  
DB 1951 GGATGGTTCGGTAATTTATAGCAACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2010  
QY 796 TGATCCACCGTGAAGCAGTGTGTTCTCTCAAGTAAATAAGTCGGTTAGTATTCATCGA 855

DB 2011 TGATCCACCGTGAAGCAGTGTGTTCTCTCAAGTAAATAAGTCGGTTAGTATTCATCGA 2070  
QY 856 TTGGAGCC 863  
DB 2071 TTGGAGCC 2078  
RESULT 12  
AY485644.2/c  
WPCOMMENT  
Sequence split into 5 fragments LOCUS AY485644 Accession AY485644  
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AY485644\_3 300001 410000  
AY485644\_4 400001 438828  
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Best Local Similarity 77.4%; Pred. No. 9e-76; Mismatches 62; Indels 64; Gaps 1;  
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QY 496 GACACAGAGATGATGGTGGGGCTGCCCATTTATCCCAATGCAGGAGAGACGCGAAG 555  
DB 54160 GACACAGAGATGATGGTGGGGCTGCCCATTTATCTGACGATGCAGGAGAGACGCGAAG 54101  
QY 556 GTGATGAGGTATAGGAG 615  
DB 54100 GTGATGAGGTATAGGAG 54041  
QY 616 TCCAGAAAGCTTACGCTGAGCTTCGGCCATCGGTCACGCGCGCTTTGTCAAGGTACCC 675  
DB 54040 TCCAGAAAGCTTACGCGAGCTCAGGCCACGGTCAATGGCTGCTTTGTCAAGGTACCA 53981  
QY 676 GAAGCCATGGCATCGCCATCATCTCCAGCTTCGCCCTATGATCCTAGTAAACTTCACCTC 735  
DB 53980 GAAGCGCTGCATCGTCTGCCCTATGATCCTAGTAAACTTCACCTC 53921  
QY 736 GGATGGTTCGGTAATTTATAGCAACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 795  
DB 53920 GGATGGTTCAGTGTGTT----- 53903  
QY 796 TGATCCACCGTGAAGCAGTGTGTTCTCTCAAGTAAATAAGTCGGTTAGTATTCATCGA 855  
DB 53902 -----TTTCATCAAGTAAATAAGTGTGTTATTTGATTCACCGA 53865  
QY 856 TTGGAGCCATTATGTTGACTTTGACTATTATAAATGGTGCAGGAGATCAATCAACAAAATG 915  
DB 53864 CGGAGGAGTATGTTGATTTGACTATTTTCAAAAGTGCAGCAACCAATCAAGAAAATG 53805  
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DB 53804 TATTTGTTGAAACAAGTATTCCTTTATGTTTAAATTTAAGCATGTAAATTTGAGGAGG 53745  
QY 976 ATAGCTACTTTGATGTGT 993  
DB 53744 CTAGCTACTTAGTGTGT 53727  
RESULT 13  
AY485980  
LOCUS AY485980 1790 bp DNA linear PLN 17-MAR-2004  
DEFINITION Triticum turgidum cultivar Langdon ZCCT2-Td (VRN2) gene, complete  
cds.  
ACCESSION AY485980  
VERSION AY485980.1 GI:45390748  
KEYWORDS

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SOURCE      Triticum turgidum
ORGANISM    Triticum turgidum
DEFINITION  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
              Poideae; Triticeae; Triticum.
REFERENCE   1 (bases 1 to 1790)
AUTHORS    Yan, L., Loukolanov, A., Blechl, A., Tranquilli, G., Ramakrishna, W.,
              SanMiguel, P., Bennetzen, J.L., Echenique, V. and Dubcovsky, J.
TITLE      The Wheat VRN2 Gene Is a Flowering Repressor Down-Regulated by
              Vernalization
JOURNAL    Science 303 (5664), 1640-1644 (2004)
PUBMED     15016992
REFERENCE   2 (bases 1 to 1790)
AUTHORS    Yan, L., Loukolanov, A., Blechl, A., Tranquilli, G., Ramakrishna, W.,
              SanMiguel, P., Bennetzen, J.L., Echenique, V. and Dubcovsky, J.
TITLE      Direct Submission
JOURNAL    Submitted (20-NOV-2003) Agronomy and Range Science, University of
              California, One Shields Avenue, Davis, CA 95616, USA
FEATURES   Location/Qualifiers
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               YDKQIRYESRKAYAEELRVNGRFVKVPEAAASSPPSPDPSKLHLGWF"

gene
mRNA
CDS

ORIGIN
Query Match      26.8%; Score 267.2; DB 15; Length 1790;
Best Local Similarity 86.0%; Pred. No. 1.8e-61;
Matches 296; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

QY 436 GTGCCATTTCAGGAGTGCATTCACCAACACTATTAGCAATGAAGCAATCATGACTATT 495
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QY 496 GACACAGATCATGTGGGGCTGCCCATTTATCCACAATGCAGAGAGAGAGAGAGAG 555
DB 1491 GATACAGATCATGTGGGGCTGCCCATTAATCTGACGATGAGAGAGAGAGAGAGAG 1550
QY 556 GTGATGAGGTATAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 615
DB 1551 GTGATGAGGTATAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1610
QY 616 TCCAGAAAGCTTACGCTGAGCTTCGGCCATGGGTCAACGGCGCTTTGTCAAGTACCC 675
DB 1611 TCCAGAAAGCTTACGCTGAGCTTCGGCCATGGGTCAACGGCGCTTTGTCAAGTACCA 1670
QY 676 GAAGCCATGGCATCGGCATCATCTCCAGCTTCGCCCTATGATCCTAGTAACTTCACTTC 735
DB 1671 GAAGCCGCTGATCTGCTGCTACCCCGAGCTTCGCCCTATGATCCTAGTAACTTCACTTC 1730
QY 736 GGATGGTTCGGTAATTTATAGCACAAGCCAGATATAAATGATAA 779
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RESULT 14

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AY485978    2064 bp      DNA      linear      PLN 17-MAR-2004
LOCUS       Hordeum vulgare cultivar Bairokkaku ZCCT-Hb (VRN2) gene, partial
DEFINITION  cds.
ACCESSION   AY485978
VERSION     AY485978.1 GI:45390740
KEYWORDS    Hordeum vulgare
SOURCE      Hordeum vulgare
ORGANISM    Hordeum vulgare
REFERENCE   1 (bases 1 to 2064)
AUTHORS    Yan, L., Loukolanov, A., Blechl, A., Tranquilli, G., Ramakrishna, W.,
              SanMiguel, P., Bennetzen, J.L., Echenique, V. and Dubcovsky, J.
TITLE      The Wheat VRN2 Gene Is a Flowering Repressor Down-Regulated by
              Vernalization
JOURNAL    Science 303 (5664), 1640-1644 (2004)
PUBMED     15016992
REFERENCE   2 (bases 1 to 2064)
AUTHORS    Yan, L., Loukolanov, A., Blechl, A., Tranquilli, G., Ramakrishna, W.,
              SanMiguel, P., Bennetzen, J.L., Echenique, V. and Dubcovsky, J.
TITLE      Direct Submission
JOURNAL    Submitted (20-NOV-2003) Agronomy and Range Science, University of
              California, One Shields Avenue, Davis, CA 95616, USA
FEATURES   Location/Qualifiers
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gene
mRNA
CDS

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Best Local Similarity 88.3%; Pred. No. 4e-57;
Matches 273; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

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DB 1756 GTGCCATTTCGCGGAGTGCATTCACCAACACTATTAGCAACGCAACGATCATGACTATT 1815
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DB 1816 GATACAGATCATGTGGGGCTGCCCATTAATCTGACGATGAGAGAGAGAGAGAGAG 1875
QY 556 GTGATGAGGTATAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 615
DB 1876 GTGATGAGGTATAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1935
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DB 1936 TCCAGAAAGCTTACGCTGAGCTTAGGCCACGGGTCAACGGCGCTTTGTCAAGTACCT 1995
QY 676 GAAGCCATGGCATCGGCATCATCTCCAGCTTCGCCCTATGATCCTAGTAACTTCACTTC 735
DB 1996 GAAGCCGCTGGTTCACCATCACCCCGAGCTTCGCCCGCATGATCCTAGTAACTTCACTTC 2055

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QY 736 GGATGCTTC 744
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Db 2056 GGATGCTTC 2064

RESULT 15
AY485977
LOCUS AY485977
DEFINITION Hordeum vulgare cultivar Dairokkaku ZCCT-Ha (VRN2) gene, partial cds.
ACCESSION AY485977
VERSION AY485977.1 GI:45390737
KEYWORDS
SOURCE Hordeum vulgare
ORGANISM Hordeum vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticeae; Hordeum.
REFERENCE 1 (bases 1 to 1985)
AUTHORS Yan,L., Loukianov,A., Blechl,A., Tranquilli,G., Ramakrishna,W.,
SanWiguel,P., Bennetzen,J.L., Echenique,V. and Dubcovsky,J.
TITLE The Wheat VRN2 Gene Is a Flowering Repressor Down-Regulated by
Vernalization
JOURNAL Science 303 (5664), 1640-1644 (2004)
PUBMED 15016992
REFERENCE 2 (bases 1 to 1985)
AUTHORS Yan,L., Loukianov,A., Blechl,A., Tranquilli,G., Ramakrishna,W.,
SanWiguel,P., Bennetzen,J.L., Echenique,V. and Dubcovsky,J.
TITLE Direct Submission
JOURNAL Submitted (20-NOV-2003) Agronomy and Range Science, University of
California, One Shields Avenue, Davis, CA 95616, USA
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Query Match 24.9%; Score 247.6; DB 15; Length 1985;
Best Local Similarity 81.0%; Pred. NO. 4.3e-56;
Matches 342; Conservative 0; Mismatches 64; Indels 16; Gaps 4;

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Db 238 CTGCTCTTCTTCTTCTTCTTCTCGATCTCTCTTCCAG-----CACCAGACACACAGAA 291

QY 64 CAGAAAAACAAACAGCAAGCAAACTTGGAGCTAGCTAGCAGTATGTCCATGTCATGC 123
Db 292 ACAACAACTAGCAACAAAGCAAGCTTGGAGTTAGCT-GCAGTATGTCCATGTCATGT 350

QY 124 GGTGTTGGCGGCGCAACAACTCGCGCGCTCTAGGTCGCGCATTTCCATCATCAT 183
Db 351 GGTGTTGGCGGCGCAACAACTCGCGCTTACCATGATGTCGCGCTTCTTCTTCTCAT 410

QY 184 CACCATCATCAGAGACACAGCTGTGTGAGTACCAGTCTTCTGCCCATGCCAACACAC 243
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Job time : 5419 secs

GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 23, 2006, 11:51:16 ; Search time 714 Seconds

(without alignments)  
9296.986 Million cell updates/sec

Title: US-10-723-947-75

Perfect score: 996

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Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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1: Geneseqn1980s.\*

2: Geneseqn1990s.\*

3: Geneseqn2000s.\*

4: Geneseqn2001as.\*

5: Geneseqn2001bs.\*

6: Geneseqn2002as.\*

7: Geneseqn2002bs.\*

8: Geneseqn2003as.\*

9: Geneseqn2003bs.\*

10: Geneseqn2003cs.\*

11: Geneseqn2003ds.\*

12: Geneseqn2004as.\*

13: Geneseqn2004bs.\*

14: Geneseqn2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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1	996	100.0	996	13	ADS19577	Ads19577 One grain
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3	561	56.3	7051	13	ADS19576	Ads19576 One grain
4	553	55.5	2913	13	ADS19580	Ads19580 Langdon (
5	455.2	45.7	642	13	ADS19593	Ads19593 Winter ba
6	451.4	45.3	639	13	ADS19587	Ads19587 Langdon (
7	449	45.1	639	13	ADS19590	Ads19590 Winter ba
8	445	44.7	639	13	ADS19584	Ads19584 One grain
9	320.8	32.2	3454	13	ADS19586	Ads19586 Langdon (
10	320.8	32.2	5734	13	ADS19583	Ads19583 One grain
11	251.4	25.2	2043	13	ADS19592	Ads19592 Winter ba
12	247.6	24.9	1985	13	ADS19589	Ads19589 Winter ba
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14	93	9.3	1078	13	ADS16786	Ads16786 Lhd4-rela
15	93	9.3	1078	13	ADS16783	Ads16783 Lhd4-rela
16	93	9.3	2723	13	ADS16785	Ads16785 Lhd4-rela
17	93	9.3	2723	13	ADS16779	Ads16779 Lhd4-rela
18	93	9.3	2723	13	ADS16782	Ads16782 Lhd4-rela
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21	76.6	7.7	1120	12	ADO02184	Ado02184 Thalecres
22	76.6	7.7	1125	3	AAC47873	Aac47873 Arabidops
23	76.6	7.7	1127	3	AAC45341	Aac45341 Arabidops
24	76.6	7.7	1141	10	ADB31874	Adb31874 DNA encod
25	75.4	7.6	577	12	ADJ39390	Adj39390 Plant CDN
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27	74.6	7.5	1388	14	AEb65256	Aeb65256 Rice geno
28	73.6	7.4	1461	13	ADX32661	Adx32661 Plant ful
29	73.2	7.3	623	3	AAW78441	Aaw78441 Plant SDF
30	72.2	7.2	388	10	ADK54130	Adk54130 Plant DNA
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37	70	7.0	734	9	ADA49038	Ada49038 Wheat gen
38	70	7.0	734	10	ADC03443	Adc03443 Wheat flo
39	70	7.0	734	11	ACL32613	Ac132613 Rice abio
40	70	7.0	1132	13	ADX50712	Adx50712 Plant ful
41	70	7.0	1229	13	ADX47569	Adx47569 Plant ful
42	69.4	7.0	596	13	ACN60093	Acn60093 Cotton gy
43	68.4	6.9	533	13	ACN61587	Acn61587 Cotton gy
44	65.2	6.6	1728	14	ADM16414	Adm16414 E Grandis
45	65.8	6.6	699	9	ADA48119	Ada48119 Rice gene

## ALIGNMENTS

### RESULT 1

ADS19577  
ID ADS19577 standard; cDNA; 996 BP.

XX ADS19577;

XX 30-DEC-2004 (first entry)

DE One grained wheat DW92 ZCCT1 cDNA.

XX One grained wheat; chromosome 5a; ss; APETALAI; API; vernalisation;

KW flowering; ZCCT1; ZCCT2; vrnl; vrn2; CARG box; plant; gene.

XX Triticum monococcum.

OS US2004205848-A1.

XX 14-OCT-2004.

XX 26-NOV-2003; 2003US-00723947.

XX 11-APR-2003; 2003US-00412137.

XX (REGC ) UNIV CALIFORNIA.

PA Dubcovsky J, Yan L, Loukoianov A;

XX WPI; 2004-728059/71.

XX P-PSDB; ADS19578.

XX New recombinant ZCCT1 protein coding sequence useful for altering a plant's (e.g., wheat, barley, rye, oats, or forage grasses) response to vernalization or flowering times.

XX Claim 1; SEQ ID NO 75; 115pp; English.

XX The invention relates to a recombinant ZCCT1 protein (Zn finger and CCT domain protein) coding sequence comprising a nucleic acid that hybridizes to the barley ZCCT1 cDNA appearing as ADS19577. The patent also discloses the identification of to genes, vrnl identified as API (APETALAI) and vrn2 identified as ZCCT1 controlling vernalisation of flowering in temperate grasses. ZCCT1 also has a duplicate gene ZCCT2, all three genes



have been localised to chromosome 5a of one grained wheat, *Triticum monococcum*. ZCCT1 is the repressor of AP1 whose promoter contains a binding site for ZCCT1 termed the CARG box. Also included are a vector comprising the recombinant ZCCT1 protein coding sequence above, a cell comprising the vector, a transgenic plant comprising the recombinant ZCCT1 protein coding sequence above (or a genetic construct that inhibits ZCCT1 repression of AP1), a seed from the transgenic plant, a method for altering a plant's response to vernalisation and a molecular marker for vrn2 derived from AD319577. The genetic construct is an interference RNA construct (RNAi) that inhibits ZCCT1 activity and comprises an antisense construct that inhibits ZCCT1 activity, a nucleic acid sequence encoding a repression defective ZCCT1 protein operably linked to a promoter or a nucleic acid sequence encoding a DNA binding defective ZCCT1 protein operably linked to a promoter. The present sequence is a plant ZCCT1 cDNA sequence.

Query Match	100.0%;	Score 996;	DB 13;	Length 996;
Best Local Similarity	100.0%;	Pred. No. 6e-288;		
Matches 996; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0

Qy		1	TAACTGCGCTTCTTTCTTCCTCGAGCGTCTCTCCTCGGTCTCTCAACGCACAGACCA	60
Db		1	TAACTGCGCTTCTTTCTTCCTCGAGCGTCTCTCCTCGGTCTCTCAACGCACAGACCA	60
Qy		61	CACCAGAAAAAACAACAAGCAAACCTTGAGAGCTAGCTAGCAGTATGTCCATGTCA	120
Db		61	CACCAGAAAAAACAACAAGCAAACCTTGAGAGCTAGCTAGCAGTATGTCCATGTCA	120
Qy		121	TGCGGTTGTGCGGCCAACAAACTGGCCGCGCTCATGCTTGCCCCATTCCACCATCAT	180
Db		121	TGCGGTTGTGCGGCCAACAAACTGGCCGCGCTCATGCTTGCCCCATTCCACCATCAT	180
Qy		181	GATCACCATCATCAGSAGCAACGAGTGTGAGTACCAGTTCTTCGCCCATGSCAACCAAC	240
Db		181	CATCACCATCATCAGSAGCAACGAGTGTGAGTACCAGTTCTTCGCCCATGSCAACCAAC	240
Qy		241	CACCACCAACCATGGTTCGGCAGCAGATACCCAGTGCACCGCGCCGACAGCAACTTC	300
Db		241	CACCACCAACCATGGTTCGGCAGCAGATACCCAGTGCACCGCGCCGACAGCAACTTC	300
Qy		301	GACCACCGCAGAACAATGAACAGACCAATTTTCATGAAAACAGCAGCGCGGAGGAAACAGCAGC	360
Db		301	GACCACCGCAGAACAATGAACAGACCAATTTTCATGAAAACAGCAGCGCGGAGGAAACAGCAGC	360
Qy		361	AGGCTCACGCTGGAGGTGGGCGAGCGGCCAAACACATGGCTCACCTAGTGCAGCCACCG	420
Db		361	AGGCTCACGCTGGAGGTGGGCGAGCGGCCAAACACATGGCTCACCTAGTGCAGCCACCG	420
Qy		421	GCAAGAGCCCACATCGTGCCATTTTCAGSGAGTGTCATTCACCAACACTATTAGCAATGAA	480
Db		421	GCAAGAGCCCACATCGTGCCATTTTCAGSGAGTGTCATTCACCAACACTATTAGCAATGAA	480
Qy		481	GCAATCATGACTATTGACACAGAGATGATGGTGGGGCTGCCATTATCCCAAAATGCAG	540
Db		481	GCAATCATGACTATTGACACAGAGATGATGGTGGGGCTGCCATTATCCCAAAATGCAG	540
Qy		541	GAGAGAGCGAAGGTTCATGAGTATAGGAGAGAGAGAGGCGGGCGCTATGACAG	600
Db		541	GAGAGAGCGAAGGTTCATGAGTATAGGAGAGAGAGAGGCGGGCGCTATGACAG	600
Qy		601	CAAAATCCGATACGAGTCCAGAAAAGCTTTACGCTGAGCTTCGGGCATGGGGTCAACGGCCGC	660
Db		601	CAAAATCCGATACGAGTCCAGAAAAGCTTTACGCTGAGCTTCGGGCATGGGGTCAACGGCCGC	660
Qy		661	TTTGTCAAAGGTACCGAAGCCATGGCATFCGCCATCATCTCCAGCTTCGCCCTATGATCT	720
Db		661	TTTGTCAAAGGTACCGAAGCCATGGCATFCGCCATCATCTCCAGCTTCGCCCTATGATCT	720
Qy		721	AGTAAACTTCACCTCGGATGGTTCGGGTAAATTTATAGCAAAAGCCAGATAAAATGATAC	780
Db		721	AGTAAACTTCACCTCGGATGGTTCGGGTAAATTTATAGCAAAAGCCAGATAAAATGATAC	780



QY 496 GACACAGAGATGATGGTGGGGCTGCCCATTTATCCCAATCCAGAGAGACGCGAAG 555  
 |||||  
 Db 4642 GACACAGAGATGATGGTGGGGCTGCCCATTTATCCCAATCCAGAGAGACGCGAAG 4701  
 |||||  
 QY 556 GTGATGAGTATAGGAG 615  
 |||||  
 Db 4702 GTGATGAGTATAGGAG 4761  
 |||||  
 QY 616 TCCAGAAAAGCTTACGCTGAGCTTCGGCCATGGGTCAACGGCGCTTTGTCAAGGTACCC 675  
 |||||  
 Db 4762 TCCAGAAAAGCTTACGCTGAGCTTCGGCCATGGGTCAACGGCGCTTTGTCAAGGTACCC 4821  
 |||||  
 QY 676 GAAGCCATGGCATCGCCATCATCTCAGCTTCGCCCTATGATCCTAGTAAATTCACCTC 735  
 |||||  
 Db 4822 GAAGCCATGGCATCGCCATCATCTCAGCTTCGCCCTATGATCCTAGTAAATTCACCTC 4881  
 |||||  
 QY 736 GGATGGTCCGGTAAATTTATAGCAGAGCCAGATAAATGATGAATTTTCTCTGAT 795  
 |||||  
 Db 4882 GGATGGTCCGGTAAATTTATAGCAGAGCCAGATAAATGATGAATTTTCTCTGAT 4941  
 |||||  
 QY 796 TGATCCACCCGTAAGCAGAGTCTTCTCTCAAGTAAATTAAGTCGGTTAGTGATTCGCA 855  
 |||||  
 Db 4942 TGATCCACCCGTAAGCAGAGTCTTCTCTCAAGTAAATTAAGTCGGTTAGTGATTCGCA 5001  
 |||||  
 QY 856 TTGGAGCCATTAATGTTGACTTGACTATTTAAATAGTGGTGGAGATCAATCAAAATG 915  
 |||||  
 Db 5002 TTGGAGCCATTAATGTTGACTTGACTATTTAAATAGTGGTGGAGATCAATCAAAATG 5061  
 |||||  
 QY 916 TATTTATTGAACAAGTCTTGTATTACTACGTTGATTAAACATGTAATTTCAAGAGG 975  
 |||||  
 Db 5062 TATTTATTGAACAAGTCTTGTATTACTACGTTGATTAAACATGTAATTTCAAGAGG 5121  
 |||||  
 QY 976 ATAGTACTTTTGATGTGAAT 996  
 |||||  
 Db 5122 ATAGTACTTTTGATGTGAAT 5142  
 |||||

## RESULT 4

ADSI19580  
 ID ADS19580 standard; DNA; 2913 BP.  
 XX  
 AC ADS19580;  
 XX  
 DT 30-DEC-2004 (first entry)  
 XX  
 DE Langdon (tetraploid) wheat ZCCT1 genomic DNA.  
 XX  
 KW Wild emmer wheat; ds; APETAL1; AP1; vernalisation; flowering; ZCCT1;  
 ZCCT2; vrn1; vrn2; CARG box; plant; gene.  
 XX  
 OS Triticum turgidum; subsp. dicoccoides.  
 XX  
 FN US2004205848-A1.  
 XX  
 PD 14-OCT-2004.  
 XX  
 PF 26-NOV-2003; 2003US-00723947.  
 XX  
 PR 11-APR-2003; 2003US-00412137.  
 XX  
 PA (REGC ) UNIV CALIFORNIA.  
 XX  
 PI Dubcovsky J, Yan L, Loukolanov A;  
 XX  
 DR WPI; 2004-728059/71.  
 DR P-FSDB; ADS19582.  
 XX  
 PT New recombinant ZCCT1 protein coding sequence useful for altering a  
 plant's (e.g., wheat, barley, rye, oats, or forage grasses) response to  
 vernalization or flowering times.  
 XX  
 PS Disclosure; SEQ ID NO 78; 115pp; English.  
 XX

CC The invention relates to a recombinant ZCCT1 protein (Zn finger and CCT  
 domain protein) coding sequence comprising a nucleic acid that hybridises  
 CC to the barley ZCCT1 cDNA appearing as ADS19577. The patent also discloses  
 CC the identification of to genes, vrn1 identified as AP1 (APETAL1) and  
 CC vrn2 identified as ZCCT1 controlling vernalisation of flowering in  
 CC temperate grasses. ZCCT1 also has a duplicate gene ZCCT2, all three genes  
 CC have been localised to chromosome 5a of one grained wheat, triticum  
 CC monococcum. ZCCT1 is the repressor of AP1 whose promoter contains a  
 CC binding site for ZCCT1 termed the CARG box. Also included are a vector  
 CC comprising the recombinant ZCCT1 protein coding sequence above, a cell  
 CC comprising the vector, a transgenic plant comprising the recombinant  
 CC ZCCT1 protein coding sequence above (or a genetic construct that inhibits  
 CC ZCCT1 repression of AP1), a seed from the transgenic plant, a method for  
 CC altering a plant's response to vernalisation and a molecular marker for  
 CC vrn2 derived from ADS19577. The genetic construct is an interference RNA  
 CC construct (RNAi) that inhibits ZCCT1 activity and comprises an antisense  
 CC construct that inhibits ZCCT1 activity, a nucleic acid sequence encoding  
 CC a repressor defective ZCCT1 protein operably linked to a promoter or a  
 CC nucleic acid sequence encoding a DNA binding defective ZCCT1 protein  
 CC operably linked to a promoter. The present sequence is a plant ZCCT  
 CC genomic DNA sequence.  
 XX

SEQ Sequence 2913 BP; 867 A; 627 C; 575 G; 844 T; 0 U; 0 Other;

Query Match 55.5%; Score 553; DB 13; Length 2913;  
 Best Local Similarity 99.1%; Pred. No. 1.2e-154;  
 Matches 556; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 436 GTGCCATTTTCCAGGAGGTGCATTCCACCAACTATTAGCAATGAAGCAATCATGACTATT 495  
 |||||  
 Db 2133 GTGCCATTTTCCAGGAGGTGCATTCCACCAACTATTAGCAATGAAGCAATCATGACTATT 2192  
 |||||  
 QY 496 GACACAGAGATGATGGTGGGGCTTCCCATTTATCCCAATGCAGGAGAGACGCGAAG 555  
 |||||  
 Db 2193 GACACAGAGATGATGGTGGGGCTTCCCATTTATCCCAATGCAGGAGAGACGCGAAG 2252  
 |||||  
 QY 556 GTGATGAGTATAGGAG 615  
 |||||  
 Db 2253 GTGATGAGTATAGGAG 2312  
 |||||  
 QY 616 TCCAGAAAAGCTTACGCTGAGCTTCGGCCATGGGTCAACGGCGCTTTGTCAAGGTACCC 675  
 |||||  
 Db 2313 TCCAGAAAAGCTTACGCTGAGCTTCGGCCATGGGTCAACGGCGCTTTGTCAAGGTACCC 2372  
 |||||  
 QY 676 GAAGCCATGGCATCGCCATCATCTCAGCTTCGCCCTATGATCCTAGTAAATTCACCTC 735  
 |||||  
 Db 2373 GAAGCCATGGCATCGCCATCATCTCAGCTTCGCCCTATGATCCTAGTAAATTCACCTC 2432  
 |||||  
 QY 736 GGATGGTCCGGTAAATTTATAGCAGAGCCAGATAAATGATGAATTTTCTCTGAT 795  
 |||||  
 Db 2433 GGATGGTCCGGTAAATTTATAGCAGAGCCAGATAAATGATGAATTTTCTCTGAT 2492  
 |||||  
 QY 796 TGATCCACCCGTAAGCAGAGTCTTCTCTCAAGTAAATTAAGTCGGTTAGTGATTCGCA 855  
 |||||  
 Db 2493 TGATCCACCCGTAAGCAGAGTCTTCTCTCAAGTAAATTAAGTCGGTTAGTGATTCGCA 2552  
 |||||  
 QY 856 TTGGAGCCATTAATGTTGACTTGACTATTTAAATAGTGGTGGAGATCAATCAAAATG 915  
 |||||  
 Db 2553 TTGGAGCCATTAATGTTGACTTGACTATTTAAATAGTGGTGGAGATCAATCAAAATG 2612  
 |||||  
 QY 916 TATTTATTGAACAAGTCTTGTATTACTACGTTGATTAAACATGTAATTTCAAGAGG 975  
 |||||  
 Db 2613 TATTTATTGAACAAGTCTTGTATTACTACGTTGATTAAACATGTAATTTCAAGAGG 2672  
 |||||  
 QY 976 ATAGTACTTTTGATGTGAAT 996  
 |||||  
 Db 2673 ATAGTACTTTTGATGTGAAT 2693  
 |||||

## RESULT 5

ADSI19593  
 ID ADS19593 standard; cDNA; 642 BP.

AC	ADSI9593;	181	CGGGCAATTGGCCACCGCAGATCATGGGCCCGCTGTTTTCATGAACAGCAGCTCCA	240
XX				
DT	30-DEC-2004 (first entry)			
XX				
DE	Winter barley ZCCT-Hb cDNA.	349	GGGAACAGCAGCAGGCTCAGCTGGAGGTGGCGGCGGCAACACATGGCTCACCTA	408
XX				
KW	Barley; ss; APETALAI; APL; vernalisation; flowering; ZCCT1; ZCCT2; vrn1;	241	GTGAATAGCACCAGGCTCACACAAGAGGTGGACGCGGCGGCAACAGATGGCTCACCTG	300
XX				
KW	vrn2; CarG box; plant; gene.	409	GTGACGACCACGG-----CAGAGCCACATCGTGCCTTTTCAGGAGGTGCAATTCACC	462
XX				
OS	Hordeum vulgare.	301	CTGCAGCCACCGCGCGCCGCAAGAGCCACCATCGTGCCATTCCGCGGAGTGCATTCACC	360
XX				
PN	US2004205848-A1.	463	AACACTATTAGCAATGAAGCAATCATGACTATTGACACAGAGATGATGGTGGGCGCTGCC	522
XX				
PN	14-OCT-2004.	361	AACACTATTAGCAACGCAACGATCATGACTATTGATACAGAGATGATGCGGGGACTGCC	420
XX				
PF	26-NOV-2003; 2003US-00723947.	523	CATTATCCCAATCGCAGGAGAGCAGGGAAGGTGATGAGGTATAGGAGAGAGAGAG	582
XX				
XX	11-APR-2003; 2003US-00412137.	421	TATAGTCCAACGATGAGGAAGAGAAAGGATGATGAGGTACAGGAGAGAGAGAG	480
XX				
XX	(REGC ) UNIV CALIFORNIA.	583	AGGCGCGCTATGACAAGCAATCCGATACGAGTCCAGAAAGCTTACGCTGAGCTTCGG	642
XX				
PI	Dubcovsky J, Yan L, Loukoianov A;	481	AAGCGCGCTATGACAAGCAATCCGATACGAGTCCAGAAAGCTTACGCTGAGCTTCGG	540
XX				
PI	WPI; 2004-728059/71.	643	CCATGGGTCAACGCGCGCTTTGTCAAGGTACCCGAGCCATGCGCATGCCATCATCTCCA	702
DR	P-PSDB; ADS19594.	541	CCACGGGTCAACGCGCGCTTTGTCAAGGTACCCGAGCCATGCGCATGCCATCATCTCCA	600
XX				
XX	New recombinant ZCCT1 protein coding sequence useful for altering a	703	GCTTCGCGCTATGATGCTTAGTAACTTCACTTCGGATGTTTC	744
PT	plant's (e.g., wheat, barley, rye, oats, or forage grasses) response to			
PT	vernalization or flowering times.	601	GCTTCGCGCTATGATGCTTAGTAACTTCACTTCGGATGTTTC	642
XX				
PS	Disclosure; SEQ ID NO 91; 115pp; English.			
XX				
CC	The invention relates to a recombinant ZCCT1 protein (Zn finger and CCT			
CC	domain protein) coding sequence comprising a nucleic acid that hybridises			
CC	to the barley ZCCT1 cDNA appearing as ADS19577. The patent also discloses			
CC	the identification of to genes, vrn1 identified as APL (APETALAI) and			
CC	vrn2 identified as ZCCT1 controlling vernalisation of flowering in			
CC	temperate grasses. ZCCT1 also has a duplicate gene ZCCT2, all three genes			
CC	have been localised to chromosome 5a of one grained wheat, Triticum			
CC	monococcum. ZCCT1 is the repressor of APL whose promoter contains a			
CC	binding site for ZCCT1 termed the CarG box. Also included are a vector			
CC	comprising the recombinant ZCCT1 protein coding sequence above, a cell			
CC	comprising the vector, a transgenic plant comprising the recombinant			
CC	ZCCT1 protein coding sequence above (or a genetic construct that inhibits			
CC	ZCCT1 repression of APL), a seed from the transgenic plant, a method for			
CC	altering a plant's response to vernalisation and a molecular marker for			
CC	vrn2 derived from ADS19577. The genetic construct is an interference RNA			
CC	construct (RNAi) that inhibits ZCCT1 activity and comprises an antisense			
CC	construct that inhibits ZCCT1 activity, a nucleic acid sequence encoding			
CC	a repressor defective ZCCT1 protein operably linked to a promoter or a			
CC	nucleic acid sequence encoding a DNA binding defective ZCCT1 protein			
CC	operably linked to a promoter. The present sequence is a plant ZCCT cDNA			
XX				
XX				
SQ	Sequence 642 BP; 165 A; 206 C; 163 G; 108 T; 0 U; 0 Other;			
	Query Match 45.7%; Score 455.2; DB 13; Length 642;			
	Best Local Similarity 83.0%; Pred. No. 1.2e-125;			
	Matches 533; Conservative 0; Mismatches 103; Indels 6; Gaps 1;			
QY	109 ATGTCCATGTCGCGTTGTGCGCGCCGCAACACTGCGCGCTCATGCTCGCC 168			
DB	1 ATGTCCATGTCGCGTTGTGCGCGCCGCAACACTGCGCGCTCATGCTCGCC 60			
QY	169 ATTACCATCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 228			
DB	61 GTTCTTCTTCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 120			
QY	229 CATGGCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCG 288			
DB	121 CAAGGTCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCG 180			
QY	289 CCAGACAACCTTGCACCAACCAACCAACCAACCAACCAACCAACCAACCAACCG 348			

Disclosure; SEQ ID NO 85; 115pp; English.

The invention relates to a recombinant ZCCT1 protein (Zn finger and CCT domain protein) coding sequence comprising a nucleic acid that hybridises to the barley ZCCT1 cDNA appearing as ADS19577. The patent also discloses the identification of to genes, vrn1 identified as APL (APETALAI) and vrn2 identified as ZCCT1 controlling vernalisation of flowering in

CC temperate grasses. ZCCT1 also has a duplicate gene ZCCT2, all three genes  
CC have been localised to chromosome 5a of one grained wheat, Triticum  
CC monococcum. ZCCT1 is the repressor of APl whose promoter contains a  
CC binding site for ZCCT1 termed the CARg box. Also included are a vector  
CC comprising the recombinant ZCCT1 protein coding sequence above, a cell  
CC comprising the vector, a transgenic plant comprising the recombinant  
CC ZCCT1 protein coding sequence above (or a genetic construct that inhibits  
CC ZCCT1 repression of APl), a seed from the transgenic plant, a method for  
CC altering a plant's response to vernalisation and a molecular marker for  
CC Vrn2 derived from ADS19577. The genetic construct is an interference RNA  
CC construct (RNAi) that inhibits ZCCT1 activity and comprises an antisense  
CC construct that inhibits ZCCT1 activity, a nucleic acid sequence encoding  
CC a repressor defective ZCCT1 protein operably linked to a promoter or a  
CC nucleic acid sequence encoding a DNA binding defective ZCCT1 protein  
CC operably linked to a promoter. The present sequence is a plant ZCCT cDNA  
CC sequence.

XX Sequence 639 BP; 161 A; 200 C; 172 G; 106 T; 0 U; 0 Other;

Query Match 45.3%; Score 451.4; DB 13; Length 639;  
Best Local Similarity 83.6%; Pred. No. 1.6e-124;  
Matches 541; Conservative 0; Mismatches 91; Indels 15; Gaps 2;

QY 109 ATGTCATCTCATCGGTTTGTGGCGGCCCAACATGCGCGGCTCATGCTTCGCGCC 168

DB 1 ATGCCCATGTCATCGGTTTGTGGCGGCCCAACATGCGCGGCTCATGCTTCGCGCC 60

QY 169 ATTACCATCATCATCACCATCATCAGGAGCACCAGCTGTGTGAGTACCAGTTCCTGCGC 228

DB 61 GTTCT-----TCAGCATCAGNACACACCGGCTGCGGAGTACCATGCTTCAC 111

QY 229 CATGGAACACACACACACCATCATGCTCGGAGCAGATACCCAGTGCACCGCG 288

DB 112 CAAGGCCACACACACACACCATCATGCTCGGAGCAGATACCCAGTGCACCGCG 171

QY 289 CCAGACACTTTCGACACCGCAGACATGAGCCAGACCATTTTCATGAACACAGCGGCA 348

DB 172 TCAGGCAATTGCAACACTGCGAGATCATGAGCACACCGTTTCATGAACACAGCGTGA 231

QY 349 GGGACAGCAGCAGGCTCACGCTGGAGGTGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 408

DB 232 GGGACAGCAGCAGGCTCACGCTGGAGGTGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 291

QY 409 GTGAGCCACCGG-----CAAGAGCCACATCGTGCCATTTACGGAGTGCATTCACC 462

DB 292 CTGCAGCCACCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 351

QY 463 RACATATTAGCAATGAAGCATCATGACTATTGACACAGATGATGTTGGGCGCTGCC 522

DB 352 AGCACTATTAGCAATGCAACGATCATGACTATTGATACAGATGATGTTGGGCGCTGCC 411

QY 523 CATTATCCACAAATGACGAGAGAGCAGCGAAGGTGATGAGGTATAGGAGAGAGGAG 582

DB 412 CATAATCTGACATGACGAGAGAGAGGCGAAGGTGATGAGGTATAGGAGAGAGGAG 471

QY 583 AGCGCGGCTATGACAAAGCAATCCGATACGAGTCCAGAAAAGCTTACGCTGAGTTCGG 642

DB 472 AGCGGCTGCTATGACAAAGCAATCCGATATGATGATCCAGAAAAGCTTACGCGAGTCA 531

QY 643 CCATGGGTCAACGGCGGCTTTGTAAGGTACCGGAAGCCATGGCATTCGCTCATCTCA 702

DB 532 CCACGGGTCAATGGCGGCTTTGTAAGGTACCGGAAGCCGCTGCTCATCTGCTCAACCCCA 591

QY 703 GCTTCGCCCTATGCTTAGTAACTTACCTCGGATGCTTCGGTGA 749

DB 592 GCTTCGCCCTATGCTTAGTAACTTACCTCGGATGCTTCGGTGA 638

RESULT 7

ADS19590

ID ADS19590 standard; cDNA; 639 BP.

XX

AC ADS19590;

XX 30-DEC-2004 (first entry)  
XX Winter barley ZCCT-Ha cDNA.

XX Barley; ss; APETALA1; APl; vernalisation; flowering; ZCCT1; ZCCT2; vrn1;  
XX vrn2; CARg box; plant; gene.

XX Hordeum vulgare.

XX US2004205848-A1.

XX 14-OCT-2004.

XX 26-NOV-2003; 2003US-00723947.

XX 11-APR-2003; 2003US-00412137.

XX (REGC ) UNIV CALIFORNIA.

XX Dubcovsky J, Yan L, Loukoianov A;

XX WPI: 2004-728059/71.

XX P-PSDB; ADS19591.

XX New recombinant ZCCT1 protein coding sequence useful for altering a  
XX plant's (e.g., wheat, barley, rye, oats, or forage grasses) response to  
XX vernalization or flowering times.

XX Disclosure; SEQ ID NO 88; 115pp; English.

XX The invention relates to a recombinant ZCCT1 protein (Zn finger and CCT  
XX domain protein) coding sequence comprising a nucleic acid that hybridises  
XX to the barley ZCCT1 cDNA appearing as ADS19577. The patent also discloses  
XX the identification of to genes, vrn1 identified as APl (APETALA1) and  
XX vrn2 identified as ZCCT1 controlling vernalisation of flowering in  
XX temperate grasses. ZCCT1 also has a duplicate gene ZCCT2, all three genes  
XX have been localised to chromosome 5a of one grained wheat, Triticum  
XX monococcum. ZCCT1 is the repressor of APl whose promoter contains a  
XX binding site for ZCCT1 termed the CARg box. Also included are a vector  
XX comprising the recombinant ZCCT1 protein coding sequence above, a cell  
XX comprising the vector, a transgenic plant comprising the recombinant  
XX ZCCT1 protein coding sequence above (or a genetic construct that inhibits  
XX ZCCT1 repression of APl), a seed from the transgenic plant, a method for  
XX altering a plant's response to vernalisation and a molecular marker for  
XX Vrn2 derived from ADS19577. The genetic construct is an interference RNA  
XX construct (RNAi) that inhibits ZCCT1 activity and comprises an antisense  
XX construct that inhibits ZCCT1 activity, a nucleic acid sequence encoding  
XX a repressor defective ZCCT1 protein operably linked to a promoter or a  
XX nucleic acid sequence encoding a DNA binding defective ZCCT1 protein  
XX operably linked to a promoter. The present sequence is a plant ZCCT cDNA  
XX sequence.

XX Sequence 639 BP; 164 A; 208 C; 159 G; 108 T; 0 U; 0 Other;

Query Match 45.1%; Score 449; DB 13; Length 639;

Best Local Similarity 84.5%; Pred. No. 8.5e-124;

Matches 545; Conservative 0; Mismatches 85; Indels 15; Gaps 3;

QY 109 ATGTCATGTCATCGGTTTGTGGCGGCCCAACATGCGCGGCTCATGCTTCGCGCC 168

DB 1 ATGCCCATGTCATCGGTTTGTGGCGGCCCAACATGCGCGGCTCATGCTTCGCGCC 60

QY 169 ATTACCATCATCATCACCATCATCAGGAGCACCAGCTGTGTGAGTACAGTTCCTCGCC 228

DB 61 GTTCTTCTTATCATCATCATCATCATCAGNACACCATGTCAGGATACAGTTCCTCGCC 120

QY 229 CATGGCAACACACACACCATCATGCTCGGAGCAGACTACCCAGTGCACCG--- 285

DB 121 CAAGG-----TCACCAACACACACACAGCGCGGCGGAGTACCCACCGCGCA 174

QY 286 CGCCGAGCAACTTCGACCCCGGAGAACATGGACCAACCATTCATGTAACACGAGG 345

175 CGCCAGACAATTGCCACCAACACACAGATCATGGACACCGCGTTTCATGAACACAGAGCT 234  
 346 GCAGGAAACAGCAGAGGCTTCAGCTGGAGGTGGCGGCGGCGCAACACATGGCTCAC 405  
 235 CCAGAGAACAGCAGCAGGCTTCACCGGAGGTGGACGCGAGGCGGCGCAACACATGGCTCAC 294  
 406 CTAGTCAGCCACCGG-----CAAGAGCCCAACATCGTGCCTTTTCCAGGAGGTGCATTC 459  
 295 CTGCTGACCCACCGCGCGCGCAAGACCAACATCGTGCCTTTTCCAGGAGGTGCATTC 354  
 460 ACCAACATATTAGCAATAGCAATCATGACTATTGACACAGAGATGATGGGGCT 519  
 355 GCAGCAGCTATTAGCAACCAACGATCATGACTATTGATACAGAAATGATGGGGCT 414  
 520 GCCATTATCCCAATGACGAGAGCAGCAGCAAGGTGATGAGGTATAGGAGAGAGG 579  
 415 GCTATTAATCCACGATGACGAGAGAGAGGCGAAGGTGATGAGGTACAGGAGAGAGG 474  
 580 AAGAGCGCGGCTATGACAAAGCAAAATCCGATACGAGTCCAGAAAGCTTACGCTGAGCTT 639  
 475 AAGAGCGCGGCTATGACAAAGCAAAATCCGATACGAGTCCAGAAAGCTTACGCGGAGCTC 534  
 640 CGGCCATGGGTCAACGCGCGCTTTGTCAAGGTACCCGAGCCATGCGCATCATCT 699  
 535 AGGCCACGGGTCAATGGCGCTTTGCCAAGGTGCGCGAAGCGCTTGTCTCCATCACCC 594  
 700 CCAGCTTCGCCCTATGATCCTAGTAACTTCACCTCGGATGTTTC 744  
 595 CCAACTTCCCGCATGATCCTAGTAACTTCACCTCGGATGTTTC 639

## RESULT 8

ADS19584  
 ID ADS19584 standard; cDNA; 639 BP.

AC ADS19584;  
 XX  
 XX  
 DT 30-DEC-2004 (first entry)  
 XX  
 DE One grained wheat DV92 ZCCT2 cDNA.  
 XX  
 KW One grained wheat; chromosome 5a; ss; APTALAI; APT1; vernalisation;  
 XX  
 KW flowering; ZCCT1; ZCCT2; vrnl1; vrnl2; CARG box; plant; gene.  
 XX  
 OS Triticum monococcum.  
 XX  
 PN US2004205848-A1.  
 PD 14-OCT-2004.  
 XX  
 PF 26-NOV-2003; 2003US-00723947.  
 XX  
 PR 11-APR-2003; 2003US-00412137.  
 XX  
 PA (REGC ) UNIV CALIFORNIA.  
 XX  
 PI Dubcovsky J, Yan L, Loukoianov A;  
 XX  
 DR WPI; 2004-728059/71.  
 DR P-PSDB; ADS19585.

PT New recombinant ZCCT1 protein coding sequence useful for altering a  
 PT plant's (e.g., wheat, barley, rye, oats, or forage grasses) response to  
 PT vernalization or flowering times.  
 XX  
 PS Disclosure; SEQ ID NO 82; 115pp; English.  
 XX  
 CC The invention relates to a recombinant ZCCT1 protein (Zn finger and CCT  
 CC domain protein) coding sequence comprising a nucleic acid that hybridises  
 CC to the barley ZCCT1 cDNA appearing as ADS19577. The patent also discloses  
 CC the identification of to genes, vrnl1 identified as APT1 (APTALAI) and  
 CC vrnl2 identified as ZCCT1 controlling vernalisation of flowering in  
 CC temperate grasses. ZCCT1 also has a duplicate gene ZCCT2, all three genes

CC have been localised to chromosome 5a of one grained wheat, Triticum  
 CC monococcum. ZCCT1 is the repressor of APT1 whose promoter contains a  
 CC binding site for ZCCT1 termed the CARG box. Also included are a vector  
 CC comprising the recombinant ZCCT1 protein coding sequence above, a call  
 CC comprising the vector, a transgenic plant comprising the recombinant  
 CC ZCCT1 protein coding sequence above for a genetic construct that inhibits  
 CC ZCCT1 repression of APT1, a seed from the transgenic plant, a method for  
 CC altering a plant's response to vernalisation and a molecular marker for  
 CC vrnl2 derived from ADS19577. The genetic construct is an interference RNA  
 CC construct (RNAi) that inhibits ZCCT1 activity and comprises an antisense  
 CC construct that inhibits ZCCT1 activity, a nucleic acid sequence encoding  
 CC a repression defective ZCCT1 protein operably linked to a promoter or a  
 CC nucleic acid sequence encoding a DNA binding defective ZCCT1 protein  
 CC operably linked to a promoter. The present sequence is a plant ZCCT cDNA  
 CC sequence.

XX  
 SQ Sequence 639 BP; 162 A; 197 C; 171 G; 109 T; 0 U; 0 Other;

Query Match 44.7%; Score 445; DB 13; Length 639;  
 Best Local Similarity 83.0%; Pred. No. 1.4e-122;  
 Matches 537; Conservative 0; Mismatches 95; Indels 15; Gaps 2;

QY 109 ATGTCATGTATGCGGTTTGTGCGGCGCAACAACTGCGCGGCTCATGTCTCGCC 168  
 DB 1 ATGTCATGTATGCGGTTTGTGCGGCGCAACAACTGCGCGGCTCATGTCTCGCC 60

QY 169 ATTACCATCATCATCACCATCATCAGGAGCAGCAGCTGTGTGAGTACCAGTCTTCGCC 228  
 DB 61 GT-----TCTTCAGCATCAGGAACAACACTGGCTGCGGAGTACCAGTCTTCACC 111

QY 229 CATGGCAACCAACCAACCAACCACTGGCTGCGGAGCAGACTACCCAGTGCACCGCGG 288  
 DB 112 CAAGGCGCAACCAACCAACCAACCACTGGCTGCGGAGTACCAGTGCACCGCGG 171

QY 289 CCAGACAACTTGCACCAACCGCAGAAACATGAGCAGACCACTTTTCATGAACACAGAGCGCA 348  
 DB 172 TCGGCGCAATTGCGCACTGCGAGATCATGAGCAGACCAACCGCTTTCATGAACACAGAGCTGCA 231

QY 349 GGAACACAGCAGGCTCAGCTGAGGTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 408  
 DB 232 GGAACACAGCAGGCTCAGCTGAGGTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 291

QY 409 GTGAGCGCACCGG-----CAAGAGCCCACTGCTGCGGCGGCGGCGGCGGCGGCGGCGG 462  
 DB 292 GTGAGCGCACCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 351

QY 463 AACACTATTAGCAATGAGCAATCATGACTATTGACACAGAGATGATGGGGCTCGCC 522  
 DB 352 AGCACTATTAGCAATGCAATCATGACTATTGATACAGAGATGATGGGGCTCGCC 411

QY 523 CATTTATCCCAATGACGAGGAGCAGGAGGTGATGAGGTATAGGAGAGAGAGAGAG 582  
 DB 412 CATTAATCTGAGCATGACGAGAGAGAGGCGAAGGTGATGAGGTATAGGAGAGAGAGAGAG 471

QY 583 AGGCGGCGCTATGACAAACAAATCCGATACGAGTCCAGAAAGCTTACCTGAGCTTCGG 642  
 DB 472 AGGCGGCGCTATGACAAACAAATCCGATACGAGTCCAGAAAGCTTACCTGAGCTTCGG 531

QY 643 CCATGGGTCAACGCGCGCTTTGTCAAGGTACCCGAAGCCATGGCATTCGCATCATCTCCA 702  
 DB 532 CCACGGGTCAATGGCTGCTTTGTCAAGGTACCCGAAGCCATGGCATTCGCATCATCTCCA 591

QY 703 GCTTCGCCCTATGATCCTAGTAACTTCACCTCGGATGGTTCGGTA 749  
 DB 592 GCTTCGCCCTATGATCCTAGTAACTTCACCTCGGATGGTTCGGTA 638

## RESULT 9

ADS19586  
 ID ADS19586 standard; DNA; 3454 BP.

XX  
 AC ADS19586;

30-DEC-2004 (first entry)  
 Langdon (tetraploid) wheat ZCCT2 genomic DNA.  
 Wild emmer wheat; ds; APEALAI; API; vernalisation; flowering; ZCCT1;  
 ZCCT2; vrnl; vrn2; CARG box; plant; gene.  
 Triticum turgidum; subsp. dicoccoides.  
 US2004205848-A1.  
 14-OCT-2004.  
 26-NOV-2003; 2003US-00723947.  
 11-APR-2003; 2003US-00412137.  
 (REGC ) UNIV CALIFORNIA.  
 Dubcovsky J, Yan L, Loukoianov A;  
 WPI; 2004-728059/71.  
 P-PSDB; ADS19588.  
 New recombinant ZCCT1 protein coding sequence useful for altering a  
 plant's (e.g., wheat, barley, rye, oats, or forage grasses) response to  
 vernalization or flowering times.  
 Disclosure; SEQ ID NO 84; 115pp; English.  
 The invention relates to a recombinant ZCCT1 protein (Zn finger and CCT  
 domain protein) coding sequence comprising a nucleic acid that hybridises  
 to the barley ZCCT1 cDNA appearing as ADS19577. The patent also discloses  
 the identification of to genes, vrnl identified as API (APEALAI) and  
 vrn2 identified as ZCCT1 controlling vernalisation of flowering in  
 temperate grasses. ZCCT1 also has a duplicate gene ZCCT2, all three genes  
 have been localised to chromosome 5a of one grained wheat, Triticum  
 monococcum. ZCCT1 is the repressor of API whose promoter contains a  
 binding site for ZCCT1 termed the CARG box. Also included are a vector  
 comprising the recombinant ZCCT1 protein coding sequence above, a cell  
 comprising the vector, a transgenic plant comprising the recombinant  
 ZCCT1 protein coding sequence above (or a genetic construct that inhibits  
 ZCCT1 repression of API), a seed from the transgenic plant, a method for  
 altering a plant's response to vernalisation and a molecular marker for  
 Vrn2 derived from ADS19577. The genetic construct is an interference RNA  
 construct (RNAi) that inhibits ZCCT1 activity and comprises an antisense  
 construct that inhibits ZCCT1 activity, a nucleic acid sequence encoding  
 a repressor defective ZCCT1 protein operably linked to a promoter or a  
 nucleic acid sequence encoding a DNA binding defective ZCCT1 protein  
 operably linked to a promoter. The present sequence is a plant ZCCT  
 genomic DNA sequence.  
 Query Match 32.2%; Score 320.8; DB 13; Length 3454;  
 Best Local Similarity 77.4%; Pred. No. 6.8e-85;  
 Matches 432; Conservative 0; Mismatches 62; Indels 64; Gaps 1;  
 436 GTGCCATTTCGGAGTGCATCCACACATATTAGCAATGACGATCATGACTATT 495  
 2645 GTGCCATTTCGGAGTGCATCCACACATATTAGCAATGACGATCATGACTATT 2704  
 496 GACACAGAGATGATGGTGGGGCTGCCCATTTATCCACAAATGACGAGAGACGAGAG 555  
 2705 GATACAGAGATGATGGTGGGGCTGCCCATTTATCCACAAATGACGAGAGACGAGAG 2764  
 556 GTGATGAGTATGAGGAGAGAGAGAGAGAGCGCGCTATGACAGCAAAATCCGATACGAG 615  
 2765 GTGATGAGTATGAGGAGAGAGAGAGAGAGCGCGCTATGACAGCAAAATCCGATACGAG 2824  
 616 TCCAGAAAGCTTACCTGAGTTCGGCCATCGGTCACGCGCTTTCTCAAGGTACCC 675  
 2825 TCCAGAAAGCTTACGCGGAGCTCAGGCCACGGGTCAATGGCGCTTTGTCAAGGTACCA 2884

676 GAAGCATGGCATGCCCATCATCTCCAGCTTCGCCCTATGATCCTAGTAAATTCACCTC 735  
 2885 GAAGCGCTGCATCGTCTGTCACCCCGAGCTTCGCCCTATGATCCTAGTAAATTCACCTC 2944  
 736 GGATGGTTCGGTAATTTATAGCACACAGCCAGATAAATGATAATATTTCTTCTGAT 795  
 2945 GGATGGTTCGGTAGTTT----- 2962  
 796 TGATCCACCCGTAAGCAGTGTGTTCTCAAAGTAAATAAGTCGGTTAGTATGATCGA 855  
 2963 -----TTCAACAAGTAATAAGTTGTTATTTGTTGACCGA 3000  
 856 TTGAGGACCATTTATGTTGACTTGCATTTTAAATGGTCAGCAGATCAATCAAAACAAATG 915  
 3001 TGGGAGGAGTTATGTTGATTTGACTTATTTCAAAAGGTGACGACCAATCAAAAGAAATG 3060  
 916 TATTATTGAACAAGTCTGTTATCTACTACGTTGATTAAACATGTAATTTCAAGAGG 975  
 3061 TATTGTTGAACAAGTATTGTTATGCTTTTAAATTAAGCAATGTTGAGGAGG 3120  
 976 ATAGCTACTTTGATGTGT 993  
 3121 CTAGCTACTTAGATGTGT 3138  
 RESULT 10  
 ADS19583  
 ID ADS19583 standard; DNA; 5734 BP.  
 XX  
 AC ADS19583;  
 XX  
 DT 30-DEC-2004 (first entry)  
 XX  
 DE One grained wheat DV92 ZCCT2 genomic DNA.  
 XX  
 KW One grained wheat; chromosome 5a; ds; APEALAI; API; vernalisation;  
 KW flowering; ZCCT1; ZCCT2; vrnl; vrn2; CARG box; plant; gene.  
 XX  
 OS Triticum monococcum.  
 XX  
 PN US2004205848-A1.  
 XX  
 PD 14-OCT-2004.  
 XX  
 PF 26-NOV-2003; 2003US-00723947.  
 XX  
 PR 11-APR-2003; 2003US-00412137.  
 XX  
 PA (REGC ) UNIV CALIFORNIA.  
 XX  
 PI Dubcovsky J, Yan L, Loukoianov A;  
 XX  
 DR WPI; 2004-728059/71.  
 DR P-PSDB; ADS19585.  
 XX  
 PT New recombinant ZCCT1 protein coding sequence useful for altering a  
 PT plant's (e.g., wheat, barley, rye, oats, or forage grasses) response to  
 PT vernalization or flowering times.  
 XX  
 PS Disclosure; SEQ ID NO 81; 115pp; English.  
 XX  
 CC The invention relates to a recombinant ZCCT1 protein (Zn finger and CCT  
 CC domain protein) coding sequence comprising a nucleic acid that hybridises  
 CC to the barley ZCCT1 cDNA appearing as ADS19577. The patent also discloses  
 CC the identification of to genes, vrnl identified as API (APEALAI) and  
 CC vrn2 identified as ZCCT1 controlling vernalisation of flowering in  
 CC temperate grasses. ZCCT1 also has a duplicate gene ZCCT2, all three genes  
 CC have been localised to chromosome 5a of one grained wheat, Triticum  
 CC monococcum. ZCCT1 is the repressor of API whose promoter contains a  
 CC binding site for ZCCT1 termed the CARG box. Also included are a vector  
 CC comprising the recombinant ZCCT1 protein coding sequence above, a cell  
 CC comprising the vector, a transgenic plant comprising the recombinant







ADSI19589	standard; DNA; 1985 BP.
XX AC	ADSI19589;
XX AD	30-DEC-2004 (first entry)
XX DT	Winter barley ZCCT-Ha genomic DNA.
XX DE	Barley; ds; APETALA1; API; vernalisation; flowering; ZCCT1; ZCCT2; vrn1;
XX KW	vrn2; CarG box; plant; gene.
XX KM	Hordeum vulgare.
XX OS	US20040205848-A1.
XX PN	14-OCT-2004.
XX PD	26-NOV-2003; 2003US-00723947.
XX PF	11-APR-2003; 2003US-00412137.
XX PR	(REGC ) UNIV CALIFORNIA.
XX PA	Dubcovsky J, Yan L, Loukoianov A;
XX PI	WPI; 2004-728059/71.
XX DR	P-PSDB; ADSI19591.
XX DD	New recombinant ZCCT1 protein coding sequence useful for altering a
XX PT	plant's (e.g., wheat, barley, rye, oats, or forage grasses) response to
XX PP	vernalization or flowering times.
XX PX	Disclosure; SEQ ID NO 87; 115pp; English.
XX PS	The invention relates to a recombinant ZCCT1 protein (Zn finger and CCT
XX PP	domain protein), coding sequence comprising a nucleic acid that hybridises
XX CC	to the barley ZCCT1 cDNA appearing as ADSI19577. The patent also discloses
XX CC	the identification of genes, vrn1 identified as API (APETALA1) and
XX CC	vrn2 identified as ZCCT1 controlling vernalisation of flowering in
XX CC	temperate grasses. ZCCT1 also has a duplicate gene ZCCT2, all three genes
XX CC	have been localised to chromosome 5a of one grained wheat, Triticum
XX CC	monococcum. ZCCT1 is the repressor of API whose promoter contains a
XX CC	binding site for ZCCT1 termed the CarG box. Also included are a vector
XX CC	comprising the recombinant ZCCT1 protein coding-sequence above, a cell
XX CC	comprising the vector, a transgenic plant comprising the recombinant
XX CC	ZCCT1 protein coding sequence above (or a genetic construct that inhibits
XX CC	ZCCT1 repression of API), a seed from the transgenic plant, a method for
XX CC	altering a plant's response to vernalisation and a molecular marker for
XX CC	vrn2 derived from ADSI19577. The genetic construct is an interference RNA
XX CC	construct (RNAi)that inhibits ZCCT1 activity and comprises an antisense
XX CC	construct that inhibits ZCCT1 activity, a nucleic acid sequence encoding
XX CC	a repression defective ZCCT1 protein operably linked to a promoter or a
XX CC	nucleic acid sequence encoding a DNA binding defective ZCCT1 protein
XX CC	operably linked to a promoter. The present sequence is a plant ZCCT
XX CC	genomic DNA sequence.
XX SQ	Sequence 1985 BP; 572 A; 489 C; 393 G; 531 T; 0 U; 0 Other;
XX	Query Match 24.9%; Score 247.6; DB 13; Length 1985;
XX	Best Local Similarity 81.0%; Pred. No. 4.8e-63;
XX	Matches 342; Conservative 0; Mismatches 64; Indels 16; Gaps 4;
QY	4 CTGCCTCTTCTTTCTTCCTCGAGCTCTCTCTCTCTCCGTCTCCACGCCACCACACAC 63
Db	238 CTGCTCTTCTTCTTCTTCCTCGACATCTCTCTCCAG-----CACCAACACACACGAA 291
QY	64 CAGAAAAACAACAAGCAAGCAAACTTGAGCTAGTAGTATGTCATTGCTCATGC 123
Db	292 ACAACAAAACACTAGCAAACGAACGGTGGAGTTAGCT-GCAGTATGTCATTGCTCATGT 350

ADSI19589	standard; DNA; 1985 BP.
XX AC	ADSI19589;
XX AD	30-DEC-2004 (first entry)
XX DT	Winter barley ZCCT-Ha genomic DNA.
XX DE	Barley; ds; APETALA1; API; vernalisation; flowering; ZCCT1; ZCCT2; vrn1;
XX KW	vrn2; CarG box; plant; gene.
XX KM	Hordeum vulgare.
XX OS	US20040205848-A1.
XX PN	14-OCT-2004.
XX PD	26-NOV-2003; 2003US-00723947.
XX PF	11-APR-2003; 2003US-00412137.
XX PR	(REGC ) UNIV CALIFORNIA.
XX PA	Dubcovsky J, Yan L, Loukoianov A;
XX PI	WPI; 2004-728059/71.
XX DR	P-PSDB; ADSI19591.
XX DD	New recombinant ZCCT1 protein coding sequence useful for altering a
XX PT	plant's (e.g., wheat, barley, rye, oats, or forage grasses) response to
XX PP	vernalization or flowering times.
XX PX	Disclosure; SEQ ID NO 87; 115pp; English.
XX PS	The invention relates to a recombinant ZCCT1 protein (Zn finger and CCT
XX PP	domain protein), coding sequence comprising a nucleic acid that hybridises
XX CC	to the barley ZCCT1 cDNA appearing as ADSI19577. The patent also discloses
XX CC	the identification of genes, vrn1 identified as API (APETALA1) and
XX CC	vrn2 identified as ZCCT1 controlling vernalisation of flowering in
XX CC	temperate grasses. ZCCT1 also has a duplicate gene ZCCT2, all three genes
XX CC	have been localised to chromosome 5a of one grained wheat, Triticum
XX CC	monococcum. ZCCT1 is the repressor of API whose promoter contains a
XX CC	binding site for ZCCT1 termed the CarG box. Also included are a vector
XX CC	comprising the recombinant ZCCT1 protein coding-sequence above, a cell
XX CC	comprising the vector, a transgenic plant comprising the recombinant
XX CC	ZCCT1 protein coding sequence above (or a genetic construct that inhibits
XX CC	ZCCT1 repression of API), a seed from the transgenic plant, a method for
XX CC	altering a plant's response to vernalisation and a molecular marker for
XX CC	Vrn2 derived from ADSI19577. The genetic construct is an interference RNA
XX CC	construct (RNAi)that inhibits ZCCT1 activity and comprises an antisense
XX CC	construct that inhibits ZCCT1 activity, a nucleic acid sequence encoding
XX CC	a repression defective ZCCT1 protein operably linked to a promoter or a
XX CC	nucleic acid sequence encoding a DNA binding defective ZCCT1 protein
XX CC	operably linked to a promoter. The present sequence is a plant ZCCT
XX CC	genomic DNA sequence.
XX SQ	Sequence 1985 BP; 572 A; 489 C; 393 G; 531 T; 0 U; 0 Other;
XX	Query Match 24.9%; Score 247.6; DB 13; Length 1985;
XX	Best Local Similarity 81.0%; Pred. No. 4.8e-63;
XX	Matches 342; Conservative 0; Mismatches 64; Indels 16; Gaps 4;
QY	4 CTGCCTCTTCTTTCTTCCTCGAGCTCTCTCTCTCTCGGTCTCCACGCCACCACACAC 63
Db	238 CTGCTCTTCTTCTTCTTCCTCGACATCTCTCTCCAG-----CACCAACACACACGAA 291
QY	64 CAGAAAAACAACAAGCAAGCAAACTTGAGCTAGTAGTATGTCATTGCTCATGC 123
Db	292 ACAACAAAACACTAGCAAAAGCAAAACGGTGGAGTTAGCT-GCAGTATGTCATTGCTCATGT 350



Db	770	CGCAATGGTGGAGAGGGAGGCCAAGCTGATGAGGTACAAGGAGAGGAGGAGAGAGGTS	829
Qy	591	CTATGACAAAGCAAATCCGATACGAGTCCAGAAAAGCTTACGCTGAGCTTCGGCCATGGGT	650
Db	830	CTACGAGAGCAANTCCGGTACGCTCCAGAAAAGCCTATGCCGAGATGAGGCCCGAGT	889
Qy	651	CAACGGCCGCTTTGTCAAGGTACCCGAGCCATGGCATCGCCATCATCTCCAGCTTCGCC	710
Db	890	GAGAGTCGCTTCGCCCAAAGAACCTGATCAGGAAGCTGTGCGACCGCCATCCACCTATGT	949
Qy	711	CTATGATCCTAGTAAACTTCACCTCGGATGCTTCGGTAAATTATAGCA	759
Db	950	CGATCCTAGTAGGCTTGAGCTTGACAAATGGTTTCAGATAGATAATTACA	998

Search completed: February 23, 2006, 12:16:19  
 Job time : 719 secs



NUMBER OF SEQUENCES: 31  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Nixon & Vanderhye PC  
STREET: 8th Floor, 1100 No. 6077994th Glebe Road  
CITY: Arlington  
STATE: Virginia  
COUNTRY: United States of America  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/945,056  
FILING DATE: 20-OCT-1997  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/GB95/02561  
FILING DATE: 01-NOV-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9422083.7  
FILING DATE: 02-NOV-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Ms Mary J Wilson  
REGISTRATION NUMBER: 32,955  
REFERENCE/DOCKET NUMBER: 620-17  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 816-4000  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1124 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA to mRNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Arabidopsis thaliana  
STRAIN: Landsberg erecta  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT: chromosome 5  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..1119  
US-08-945-056-1

Query Match  
Best Local Similarity 6.3%; Score 62.8; DB 3; Length 1124;  
Matches 88; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

QY 540 GGAGAGAGCAGCAAGGTGATGAGGTATAGGGAGAGAGAGAGCGCGCTATGACAA 599  
DB 912 GGACAGAGAGCCAGGCTCTGAGATACAGAGAGAGAGAGCAAGGAATTTGAGAA 971  
QY 600 GCAATCCGATACAGTCCAGAAAAGCTTACGCTCGGCGCATGGTCAACGGCG 659  
DB 972 GACATAAGGTATGCTTCGAGGAAGCATATGCAGAGATAAGACCGCGGTCAATGGCG 1031  
QY 660 CTTTGTCAAG 669  
DB 1032 GTTCGCAAG 1041

RESULT 3  
US-08-945-056-4  
Sequence 4, Application US/08945056  
Patent No. 6077994  
GENERAL INFORMATION:  
APPLICANT: Coupland, George M.  
APPLICANT: Putterill, Joanna J.  
TITLE OF INVENTION: Genetic control of flowering  
NUMBER OF SEQUENCES: 31

CORRESPONDENCE ADDRESS:  
ADDRESSEE: Nixon & Vanderhye PC  
STREET: 8th Floor, 1100 No. 6077994th Glebe Road  
CITY: Arlington  
STATE: Virginia  
COUNTRY: United States of America  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/945,056  
FILING DATE: 20-OCT-1997  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/GB95/02561  
FILING DATE: 01-NOV-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9422083.7  
FILING DATE: 02-NOV-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Ms Mary J Wilson  
REGISTRATION NUMBER: 32,955  
REFERENCE/DOCKET NUMBER: 620-17  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 816-4000  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4201 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
ORIGINAL SOURCE:  
ORGANISM: Arabidopsis thaliana  
STRAIN: Landsberg erecta  
POSITION IN GENOME:  
MAP POSITION: chromosome 5  
US-08-945-056-4

Query Match  
Best Local Similarity 6.3%; Score 62.8; DB 3; Length 4201;  
Matches 88; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

QY 540 GGAGAGAGCAGCAAGGTGATGAGGTATAGGGAGAGAGAGAGCGCGCTATGACAA 599  
DB 3819 GGACAGAGAGCCAGGCTCTGAGATACAGAGAGAGAGAGCAAGGAATTTGAGAA 3878  
QY 600 GCAATCCGATACAGTCCAGAAAAGCTTACGCTCGGCGCATGGTCAACGGCG 659  
DB 3879 GACATAAGGTATGCTTCGAGGAAGCATATGCAGAGATAAGACCGCGGTCAATGGCG 3938  
QY 660 CTTTGTCAAG 669  
DB 3939 GTTCGCAAG 3948

RESULT 4  
US-08-945-056-5  
Sequence 5, Application US/08945056  
Patent No. 6077994  
GENERAL INFORMATION:  
APPLICANT: Coupland, George M.  
APPLICANT: Putterill, Joanna J.  
TITLE OF INVENTION: Genetic control of flowering  
NUMBER OF SEQUENCES: 31  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Nixon & Vanderhye PC  
STREET: 8th Floor, 1100 No. 6077994th Glebe Road  
CITY: Arlington  
STATE: Virginia  
COUNTRY: United States of America

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)  
CURRENT APPLICATION DATA:  
FILING DATE: 20-OCT-1997  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
FILING DATE: 01-NOV-1995  
APPLICATION NUMBER: US/08/945,056  
FILING DATE: 20-OCT-1997  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
FILING DATE: 01-NOV-1995  
APPLICATION NUMBER: PCT/GB95/02561  
FILING DATE: 01-NOV-1995  
APPLICATION NUMBER: GB 9422083.7  
ATTORNEY/AGENT INFORMATION:  
NAME: Ms Mary J Wilson  
REGISTRATION NUMBER: 32,955  
REFERENCE/DOCKET NUMBER: 620-17  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 816-4000  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1101 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: YES  
ORIGINAL SOURCE:  
ORGANISM: Brassica napus  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..1098  
US-08-945-056-5

Query Match 5.9%; Score 58.8; DB 3; Length 1101;  
Best Local Similarity 63.4%; Pred. No. 3e-07;  
Matches 90; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

QY 540 GGAGAGAGCGCAAGCTGATGAGGTATAGGGAGAGAGAGAGCGCGCTTATGACAA 599  
DB 873 GGACAGAGAAGCTAGAGTCTGAGATACAGAGAGAGAGAGAGAAAGTTTGAGAA 932  
QY 600 GCAATCCGATACGAGTCCAGAAAAGCTTACGCTGAGCTTCGCCATGGTCAACGCCG 659  
DB 933 GACAATAAGGTATGCTTCAAGGAAGGCATATGCAGAGAGAGAGAGCGGATCAATGGACG 992  
QY 660 CTTTGTCAAGGTACCCGAGGCC 681  
DB 993 GTTTCGCAAGATTAGTGAACC 1014

RESULT 5  
US-08-945-056-7  
Sequence 7, Application US/08945056  
Patent No. 6077994  
GENERAL INFORMATION:  
APPLICANT: Coupland, George M.  
APPLICANT: Putterill, Joanna J.  
TITLE OF INVENTION: Genetic control of flowering  
NUMBER OF SEQUENCES: 31  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Nixon & Vandethye PC  
STREET: 8th Floor, 1100 No. 6077994th Glebe Road  
CITY: Arlington  
STATE: Virginia  
COUNTRY: United States of America  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/945,056  
FILING DATE: 20-OCT-1997  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
FILING DATE: 01-NOV-1995  
APPLICATION NUMBER: PCT/GB95/02561  
FILING DATE: 01-NOV-1995  
APPLICATION NUMBER: GB 9422083.7  
ATTORNEY/AGENT INFORMATION:  
NAME: Ms Mary J Wilson  
REGISTRATION NUMBER: 32,955  
REFERENCE/DOCKET NUMBER: 620-17  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 816-4000  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1101 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: YES  
ORIGINAL SOURCE:  
ORGANISM: Brassica napus  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..1098  
US-08-945-056-7

Query Match 5.7%; Score 57.2; DB 3; Length 1101;  
Best Local Similarity 62.7%; Pred. No. 9.2e-07;  
Matches 89; Conservative 0; Mismatches 53; Indels 0; Gaps 0;

QY 540 GGAGAGAGCGCAAGGTGATGAGGTATAGGGAGAGAGAGAGCGCGCTTATGACAA 599  
DB 873 GGACAGAGAAGCTAGAGTCTGAGATACAGAGAGAGAGAGAGAAAGTTTGAGAA 932  
QY 600 GCAATCCGATACGAGTCCAGAAAAGCTTACGCTGAGCTTCGCCATGGTCAACGCCG 659  
DB 933 GACAATAAGGTATGCTTCAAGGAAGGCATATGCAGAGAGAGAGAGCGGATCAATGGACG 992  
QY 660 CTTTGTCAAGGTACCCGAGGCC 681  
DB 993 GTTTCGCAAGATTAGTGAACC 1014

RESULT 6  
US-08-232-463-14/c  
Sequence 14, Application US/08232463  
Patent No. 5670367  
GENERAL INFORMATION:  
APPLICANT: DORNER, F.  
APPLICANT: SCHEIFLINGER, F.  
APPLICANT: FALKNER, F. G.  
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS  
NUMBER OF SEQUENCES: 52  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 1800 Diagonal Road, Suite 500  
CITY: Alexandria  
STATE: VA  
COUNTRY: USA  
ZIP: 22313-0299  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/232,463  
FILING DATE:



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; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 103758
; LENGTH: 522
; TYPE: DNA
; ORGANISM: Human
; US-09-949-016-103758

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	Query Match	4.5%;	Score 45.2;	DB 3;	Length 522;
	Best Local Similarity	54.1%;	Pred. No. 0.0027;		
	Matches	92;	Conservative	0;	Mismatches 78; Indels 0; Gaps 0
Qy	138	CAACAAC	TGCGGCGCCTCATGGTCTCGCCCATTCACCATCATCATCATCATCAGGA	197	
Db	398	CCATC	ACTTACCACCATCATCAATACACGACGACCAACACCATCATCAACACCATCTA	339	
Qy	198	GCACCAGCTGTGTAGTAC	CAGTCTTCTCGCCCATGGCAACACCAACCAACCAACCAACCATGG	257	
Db	338	CCAC	CNTACCATCATCTACCATCAGACGACATTTACACCATCATCTACCATCATCCA	279	
Qy	258	CTCGGCAGCAGACTAC	CCAGGTGCCACCGCGCGCAGACAACCTTCGACCA	307	
Db	278	CAATCAC	CAGCAGCAGCACCACCAACCAACCATCATCAACCAACCACTACCA	229	

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RESULT 10
US-09-949-016-14613/c
; Sequence 14613, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14613
; LENGTH: 30656
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(30656)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14613

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Query Match 4.5%; Score 45.2; DB 3; Length 30656;  
Best Local Similarity 54.1%; Pred. No. 0.031;  
Matches 92; Conservative 0; Mismatches 78; Indels 0; Gaps 0

QY 138 CAACAATGCCCGCGCTCATGGTCTCGCCCATTCACCATCATCATCATCATGGA 197  
DB 3723 CCATCATTACCACCATCAATCAATCACAGCAGCAGCAACCAACATCAACACCACTA 366

Qy	198	GCACCAGCTGTGTGAGTACAGATTTCTTGGCCATGGGAA	CCACAGCAGACACCAACCATGG	257
Db	3663	CCACCATCAACATCACTACCATACACGACCAATTA	CCACCATCACTACCAACCATCAACA	3604
Qy	258	CTGGCGAGCAGACTTACCAGTGGCCACCGCCGCCAGACAACTTCAGACACC	307	
Db	3603	CAATACACGAGCAGACCAACCAACCACTCAACACCAACCACTACCAACC	3554	

## RESULT 11

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RES001.11
US-09-949-016-12052
; Sequence 12052, Application US/09949016
; Patent NO. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CU001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12052
; LENGTH: 34230
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-12052

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Query Match 4.4%; Score 44; DB 3; Length 34230;  
Best Local Similarity 61.2%;  
Pred. NO. 0.077;  
Matches 71; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

Qy  
140 ACAACTGCCCGGCTCATGGTCTCGCCCATTCACCATCATCATCACCATCATCAGGACC 199  
|||  
Db  
4380 ACCACCACCAACCAACCAACAACACCATCACCAACCAACCAACCATCACCAAC 4439  
|||  
Qy  
200 ACCAGCTGTGTGATACCACTTTCTTGCCCCATGGCAACCAACCAACCAACCAACCAT 255  
|||  
Db  
4440 ACCAACCAATCACCAACCAACCAACCAATCACCAACCAACCAACCAACCAACCAT 4495  
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## RESULT 12

```

RESUL1' 12
US-10-148-806-3
; Sequence 3, Application US/10148805
; Patent No. 6762042
; GENERAL INFORMATION:
; APPLICANT: Bai, Chang
; APPLICANT: Metzger, Michael
; APPLICANT: Liu, Xiaomei
; TITLE OF INVENTION: DNA MOLECULES ENCODING HUMAN NHL, A DNA
; TITLE OF INVENTION: HELICASE
; FILE REFERENCE: 20585P
; CURRENT APPLICATION NUMBER: US/10/148,806
; CURRENT FILING DATE: 2002-06-05
; PRIOR APPLICATION NUMBER: US00/33065
; PRIOR FILING DATE: 2000-12-09
; PRIOR APPLICATION NUMBER: 60/169,970
; PRIOR FILING DATE: 1999-12-09
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 114793
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-148-806-3

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Search completed: February 23, 2006, 12:04:39  
Job time : 198 secs

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GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 23, 2006, 12:00:04 ; Search time 4762 Seconds  
(without alignments)  
9785.790 Million cell updates/sec

Title: US-10-723-947-75

Perfect score: 996

Sequence: 1 taactgcctcttcttcttc.....tagctacttgatggtgaat 996

Scoring table: IDENTITY\_NUC

Gapop 10\_0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

EST:\*

- 1: gb\_est1:\*
- 2: gb\_est2:\*
- 3: gb\_est3:\*
- 4: gb\_hic:\*
- 5: gb\_est4:\*
- 6: gb\_est5:\*
- 7: gb\_est6:\*
- 8: gb\_est7:\*
- 9: gb\_gss1:\*
- 10: gb\_gss2:\*
- 11: gb\_gss3:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
C 1	95.8	9.6	364	9	CC647520	CGPA002TH
C 2	95.8	9.6	833	9	BZ734187	OGFAQ22TC
C 3	95.8	9.6	1021	10	CL012630	ZMMBB053
C 4	94.8	9.5	761	9	CC728227	OGCCY57TM
C 5	94.8	9.5	850	9	CC685007	OGAS10TV
C 6	94.8	9.5	907	9	CC685002	OGAS10TH
C 7	94.8	9.5	1006	10	CL983403	ZMMBHa000
C 8	92.6	9.3	848	7	CV291360	aof01-5ms
C 9	91.2	9.2	864	10	CL972569	OsIFCC023
C 10	90.4	9.1	640	10	CL925503	OA_ABA003
C 11	90.4	9.1	726	9	CC879645	ZMMBB021
C 12	89	8.9	736	10	CL149066	104_329_1
C 13	88.8	8.9	741	9	BZ679381	PUBSI88TD
C 14	77.2	7.8	689	8	DN238319	MUC4LH100
C 15	77.2	7.8	1061	7	CK163737	FGAS01636
C 16	76.6	7.7	410	1	AV805290	AV805290
C 17	76.6	7.7	460	1	AV785412	AV785412
C 18	76.6	7.7	484	1	AV519830	AV519830
C 19	76.6	7.7	560	6	CD530587	06P03_Ara
C 20	76.6	7.7	631	1	AV538590	AV538590
C 21	76.6	7.7	832	8	DR749947	84-I02059
C 22	76.6	7.7	1088	4	CNS09YA6	BX841997 Arabidops

23	76.6	7.7	1113	4	CNS0A8F5	BX819991 Arabidops
24	76.6	7.7	1120	4	CNS0Y9F	BX842081 Arabidops
25	76.4	7.7	510	2	BE039045	BE039045 AB08H10_A
C 26	76.4	7.7	580	8	CX114723	CX114723 E1090003
C 27	76.2	7.7	319	6	CB684050	CB684050 OSJNE113D
C 28	75.8	7.6	465	10	CL953070	CL953070 OsIRUA005
C 29	75.8	7.6	547	7	CF954823	CF954823 1805r8ice
C 30	75.8	7.6	571	7	CF954930	CF954930 4869r8ice
C 31	75.8	7.6	648	7	CK084516	CK084516 83110r8ic
C 32	75.6	7.6	516	3	BJ455277	BJ455277 BJ455277
C 33	75.6	7.6	536	6	CA592638	CA592638 bsh1.pk00
C 34	75.6	7.6	536	6	CA592641	CA592641 bsh1.pk00
C 35	75.6	7.6	538	3	BJ447520	BJ447520 BJ447520
C 36	75.6	7.6	568	8	DN178125	DN178125 HO34L15S
C 37	75.6	7.6	841	2	BF264488	BF264488 HV_CBA000
C 38	75.4	7.6	400	8	DN185034	DN185034 HO34CO3W
C 39	75.4	7.6	500	6	CB663843	CB663843 OSJNE09D
C 40	75.4	7.6	502	7	CK036170	CK036170 34633r8ic
C 41	75.4	7.6	516	1	AU056338	AU056338 AU056338
C 42	75.4	7.6	582	6	CB686036	CB686036 OSJNEf16P
C 43	75.4	7.6	606	7	CF952821	CF952821 2789r8ice
C 44	75.4	7.6	653	6	CB684028	CB684028 OSJNEf13C
C 45	75.4	7.6	674	6	CB677083	CB677083 OSJNEf13L

ALIGNMENTS

RESULT 1  
CC647520/c  
LOCUS  
DEFINITION  
CGPA002TH ZM.0.7.1.5 KB Zea mays genomic clone ZMMBMA0351B03, linear GSS 19-JUN-2003  
genomic survey sequence.  
ACCESSION  
CC647520  
VERSION  
CC647520.1 GI:32048648  
KEYWORDS  
GSS.  
SOURCE  
Zea mays  
ORGANISM  
Zea mays  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.  
REFERENCE  
1 (bases 1 to 364)  
Whitellaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T., Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N., Consortium for Maize Genomics  
Unpublished (2002)  
Other GSSs: CGPA002TV  
Contact: Cathy Whitellaw  
TIGR  
9712 Medical Center Drive, Rockville, MD 20850, USA  
Tel: 301-838-5843  
Fax: 301-838-0208  
Email: whitellaw@tigr.org  
Seq primer: TR  
Class: methylation filtered.  
Location/Qualifiers  
source  
1..364  
/organism="Zea mays"  
/mol\_type="genomic DNA"  
/strain="B73"  
/db\_xref="taxon:4577"  
/clone="ZMMBMA0351B03"  
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Query Match 9.6%; Score 95.8; DB 9; Length 364;  
Best Local Similarity 65.6%; Pred.No. 5e-15;  
Matches 158; Conservative 0; Mismatches 77; Indels 6; Gaps 1;  
Oy 540 GGAGAGACGACGAGAGGTGATGAGGTATAGGAGAGAGAGAGCGCGCGTATGACAA 599



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QY 774 T 774
Db 36 T 36

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LOCUS CC728227 761 bp DNA linear GSS 23-JUN-2003
DEFINITION OGCCV57TM ZM_0.7_1.5_KB Zea mays genomic clone ZMMBMA0146117,
genomic survey sequence.
ACCESSION CC728227
VERSION CC728227.1 GI:32147160
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 761)
AUTHORS Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T.,
Citek,R.W., Nunberg,A., Robbins,D. and Lakey,N.
Consortium for Maize Genomics
Unpublished (2002)
OTHER GSSs: OGCCV57TC
CONTACT: Cathy Whitelaw
TIGR 9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TR
Class: methylation filtered.
FEATURES
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/strain="B73"
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/note="Vector: pBCSK-; Site 1: HincII; 0.7-1.5 kb
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Query Match 9.5%; Score 94.8; DB 9; Length 761;
Best Local Similarity 67.0%; Pred. No. 1.1e-14;
Matches 154; Conservative 0; Mismatches 67; Indels 9; Gaps 1;
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Db 540 GGACCGGAGGCGAAGGTGATCGGTACAGAGAGAGAGAGAGCGCGCTACGAGAA 481
QY 600 GCAATCCGATACGAGTCCAGAAAGCTTACGCTGAGCTTCGGCCATGCCATCAACGCGCG 659
Db 480 GCAGATTGCTACGCTTCCCGTAGCGGTACGGGAGATCGCGCGCGCTCAAGGCGCG 421
QY 660 CTTTGTCAAGGTACCGGAAG-----CCATGCGATCGCCATCATCTCCAGCTTCGCC 710
Db 420 CTTGCGCAAGGTGCGCGACGGTGATGCTCCCGCGCCACCGCGCGCGCTGCGGGGG 361
QY 711 CTATGATCCTAGTAACCTCACCTCGGATGTTCCGGTAATTATAGCAC 760
Db 360 CTACGAACCGCGCGCTCGACCTCGGATGTTCCGTTTCATAGCAACAC 311

RESULT 5
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LOCUS CC685007 850 bp DNA linear GSS 19-JUN-2003
DEFINITION OGOAS10TV ZM_0.7_1.5_KB Zea mays genomic clone ZMMBMA0340B19,
genomic survey sequence.
ACCESSION CC685007
VERSION CC685007.1 GI:32089783
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 850)
AUTHORS Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T.,
Citek,R.W., Nunberg,A., Robbins,D. and Lakey,N.
Consortium for Maize Genomics
Unpublished (2002)
OTHER GSSs: OGOAS10TH
CONTACT: Cathy Whitelaw
TIGR 9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TP
Class: methylation filtered.
FEATURES
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Best Local Similarity 67.0%; Pred. No. 1.2e-14;
Matches 154; Conservative 0; Mismatches 67; Indels 9; Gaps 1;
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QY 600 GCAATCCGATACGAGTCCAGAAAGCTTACGCTGAGCTTCGGCCATGCCATCAACGCGCG 659
Db 569 GCAGATTGCTACGCTTCCCGTAGCGGTACGGGAGATCGCGCGCGCTCAAGGCGCG 628
QY 660 CTTTGTCAAGGTACCGGAAG-----CCATGCGATCGCCATCATCTCCAGCTTCGCC 710
Db 629 CTTGCGCAAGGTGCGCGACGGTGATGCTCCCGCGCCACCGCGCGCGCTGCGGGGG 688
QY 711 CTATGATCCTAGTAACCTCACCTCGGATGTTCCGGTAATTATAGCAC 760
Db 689 CTACGAACCGCGCGCTCGACCTCGGATGTTCCGTTTCATAGCAACAC 738

RESULT 6
CC685002/c
LOCUS CC685002 907 bp DNA linear GSS 19-JUN-2003
DEFINITION OGOAS10TH ZM_0.7_1.5_KB Zea mays genomic clone ZMMBMA0340B19,
genomic survey sequence.
ACCESSION CC685002
VERSION CC685002.1 GI:32089778
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 907)
AUTHORS Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T.,
Citek,R.W., Nunberg,A., Robbins,D. and Lakey,N.
Consortium for Maize Genomics
Unpublished (2002)
OTHER GSSs: OGOAS10TH
CONTACT: Cathy Whitelaw
TIGR 9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TP
Class: methylation filtered.
FEATURES
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methylation filtered genomic DNA library"
ORIGIN
Query Match 9.5%; Score 94.8; DB 9; Length 850;
Best Local Similarity 67.0%; Pred. No. 1.2e-14;
Matches 154; Conservative 0; Mismatches 67; Indels 9; Gaps 1;
QY 540 GGAGAGCAGCGAAGTGATGAGGTATAGGAGAGAGAGAGCGCGCTATGACAA 599
Db 509 GGACCGGAGGCGAAGGTGATGCGGTACAGAGAGAGAGAGCGCGCTACGAGAA 568
QY 600 GCAATCCGATACGAGTCCAGAAAGCTTACGCTGAGCTTCGGCCATGCCATCAACGCGCG 659
Db 569 GCAGATTGCTACGCTTCCCGTAGCGGTACGGGAGATCGCGCGCGCTCAAGGCGCG 628
QY 660 CTTTGTCAAGGTACCGGAAG-----CCATGCGATCGCCATCATCTCCAGCTTCGCC 710
Db 629 CTTGCGCAAGGTGCGCGACGGTGATGCTCCCGCGCCACCGCGCGCGCTGCGGGGG 688
QY 711 CTATGATCCTAGTAACCTCACCTCGGATGTTCCGGTAATTATAGCAC 760
Db 689 CTACGAACCGCGCGCTCGACCTCGGATGTTCCGTTTCATAGCAACAC 738

```

```
COMMENT Other_GSSs: OGOAS10TV
Contact: Cathy Whitelaw
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5943
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TR
Class: methylation filtered.
Location/Qualifiers
1. .907
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone="ZMBMa0340819"
/clone_lib="ZM 0.7 1.5 KB"
/note="Vector: pBCSK-; Site_1: HincII; 0.7-1.5 kb
methylation filtered genomic DNA library"

ORIGIN
Query Match 9.5%; Score 94.8; DB 9; Length 907;
Best Local Similarity 67.0%; Pred. No. 1.2e-14;
Matches 154; Conservative 0; Mismatches 67; Indels 9; Gaps 1;
QY 540 GGAGAGAGCAGCGAAGGTGATGAGGTATAGGGAGAGAGAGAGAGCGCGCTATGACAA 599
DB 651 GGACCGGAGGCGAAGGTGATGCGGTACAGAGAGAGAGAGAGAGCGCGCTATGAGAA 592
QY 600 GCAATCCATACGAGTCCAGAAAGCTTACGCTGAGCTTCGCCATGGTCAACGCCG 659
DB 591 GCAGATTCCGCTACGCTTCCCGTAAGCGGTACGCGGAGATCGCGCGCGCTCAAGGGCG 532
QY 660 CTTTGTCAAGGTACCCGAAG-----CCATGGCATGCCATCATCTCCAGCTTCGCC 710
DB 531 CTTCCGCAAGTCCCGACGGTGATCTCCCGCGCCACAGCGCGCGCTCGGGGG 472
QY 711 CTATGATCTAGTAAACTTCACTCGGATGGTTCCGGTAAATTATAGCAC 760
DB 471 CTACGAACCGCGCGCTCGACCTCGGATGGTTCCGTTTCATAGCAAAACAC 422

RESULT 7
CL983403
LOCUS
DEFINITION ZMBMa0001121.f ZMBMa Zea mays genomic clone ZMBMa0001121 5',
Genomic survey sequence.
ACCESSION CL983403
VERSION CL983403.1 GI:52551481
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACAD
Clade; Panicoideae; Andropogoneae; Zea.
REFERENCE Ma, J., SanMiguel, P., Liu, R., Haller, K., Soderlund, C. and
Bennetzen, J.
Zea mays
ZMBB sequences
Unpublished (2004)
Contact: Jeff Bennetzen
Bennetzen Lab
The University of Georgia
Department of Genetics, C426a Life Sciences Building, Athens, GA
30602, USA
Tel: 706-542-3698
Fax: 706-583-0972
Email: maize@uga.edu
Plate: 0001 row: i column: 21
Class: BAC ends.
Location/Qualifiers
1. .1006
/organism="Zea mays"

FEATURES
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/mol_type="genomic DNA"
/cultivar="B73"
/db_xref="taxon:4577"
/clone="ZMBMa0001121"
/tissue_type="immature ear"
/dev_stage="6-8 weeks"
/lab_host="DH10B"
/clone_lib="ZMBMa"
/note="Vector: TOPOpcr4; Site_1: EcoRI; Site_2: EcoRI"

ORIGIN
Query Match 9.5%; Score 94.8; DB 10; Length 1006;
Best Local Similarity 67.0%; Pred. No. 1.2e-14;
Matches 154; Conservative 0; Mismatches 67; Indels 9; Gaps 1;
QY 540 GGAGAGAGCAGCGAAGGTGATGAGGTATAGGGAGAGAGAGAGAGCGCGCTATGACAA 599
DB 47 GCACCGGAGGCGAAGGTGATGCGGTACAGAGAGAGAGAGAGAGCGCGCTACGAGAA 106
QY 600 GCAATCCGATACGAGTCCAGAAAGCTTACGCTGAGCTTCGCCATGGTCAACGCCG 659
DB 107 GCAGATTCCGCTACGCTTCCCGTAAGCGGTACGCGGAGATCGCGCGCGCTCAAGGGCG 166
QY 660 CTTTGTCAAGGTACCCGAAG-----CCATGGCATGCCATCATCTCCAGCTTCGCC 710
DB 167 CTTCCCAAGGTGCGCGACGGTGATGCTCCCGCGCCACAGCGCGCGCTCGGGGG 226
QY 711 CTATGATCTAGTAAACTTCACTCGGATGGTTCCGGTAAATTATAGCAC 760
DB 227 CTACGAACCGCGCGCTCGACCTCGGATGGTTCCGTTTCATAGCAAAACAC 276

RESULT 8
CV291360
LOCUS
DEFINITION 848 bp mRNA linear EST 09-JUN-2005
aof01-5ms1-b04 Aof01 Asparagus officinalis cDNA clone
aof01-5ms1-b04 5', mRNA sequence.
ACCESSION CV291360
VERSION CV291360.1 GI:52577578
KEYWORDS EST.
SOURCE Asparagus officinalis (garden asparagus)
ORGANISM Asparagus officinalis
Asparagus officinalis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Asparagales;
Asparagaceae; Asparagus.
REFERENCE 1 (bases 1 to 848)
dePamphilis, C., Carlson, J., Ma, H., Soltis, D., Soltis, P.,
Oppenheimer, D., Frohlich, M., Doyle, J., Tanksley, S., Webb, M.,
Leebens-Mack, J., Landherr, L., Ilut, D., and Wall, K.
Generation of ESTs from early male inflorescences of Asparagus
officinalis
Unpublished (2004)
Contact: Claude dePamphilis or James Leebens-Mack
Mueller Laboratory
Penn State University
208 Mueller Laboratory, Department of Biology, ATTN Rm212, Penn
State University, University Park, PA 16802, USA
Tel: 814 863 6413
Fax: 814 865 9131
Email: cwd3@psu.edu or jhl10@psu.edu
The sequence provided is trimmed of vector and low quality regions.
Full sequence and original trace file are available from the Plant
Genome Network website (http://pgn.cornell.edu)
Plate: aof01-5ms1 row: b column: 04
Seq primer: M13F.
Location/Qualifiers
1. .848
/organism="Asparagus officinalis"
/mol_type="mRNA"
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/clone="aof01-5ms1-b04"
/tissue_type="male inflorescences"

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Location/Qualifiers
1. .848
/organism="Asparagus officinalis"
/mol_type="mRNA"
/db_xref="PCN:aof01-5ms1-b04"
/clone="aof01-5ms1-b04"
/tissue_type="male inflorescences"
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/lab_host="SOLR"
/clone_lib="Aofol"
/notes="Vector: pBluescript SK (+/-): Site_1: EcoRI;
Site_2: XhoI; this is a directionally cloned,
non-normalized library. This library has been generated by
the Floral Genome Project (FGP). The Floral Genome Project
is funded by NSF's Plant Genome Research Program
(DBI-0115684). More information about the project can be
obtained at http://fgp.bio.psu.edu"
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ORIGIN

Query Match 9.3%; Score 92.6; DB 7; Length 848;  
Best Local Similarity 55.9%; Pred. No. 4.8e-14;  
Matches 176; Conservative 0; Mismatches 139; Indels 0; Gaps 0;

QY 431 ACATGTCGTCATTCACGAGGTCATTCCACCACTATTAGCATGAGCAATCATCA 490  
DB 369 AGCTGATGCTTTCTCCGCGTGGCCCGCTACGTTTAGCCCTCGACCAACA 428  
QY 491 CTATTGACACAGATGATGGTGGGCTGCGCCATTATCCCAATGCGAGGAGAGCAG 550  
DB 429 ACTGCGCCACAGCCGAGGACGACCCGAGCCAAAGCGACCAACCCCGACAGAGG 488  
QY 551 CCAAGTGTAGGTATAGGGAAGAGGAGGCGGCTATGACAAAGCAAAATCCCGAT 610  
DB 489 CAAAGTGTAGGTACAAAGAGAGAGAGAGAGAAATACGAGAGCAATCCGAT 548  
QY 611 ACGAGTCCAGAAAGCTTACGTGAGCTTCGCGCCATGGGTCAAGCGCGCTTTGCAAG 670  
DB 549 ACGCTTCAAGAAAGCGTATGCGGAGATGAGCGGAGGATAAAGCGCGATTTGCAAGA 608  
QY 671 TACCCGAGCCATGCGATCGCATCATCTCCAGCTGCGCCCTATGATCTAGTAATCTC 730  
DB 609 CACCGAGACGAGCCAGCTCCGCGGTAAACCTCCGAATTATAATCAGGAGAGGTTG 668  
QY 731 ACTCGGATGGTTCC 745  
DB 669 ATTGTGATGGTACC 683

RESULT 9  
CL972569  
LOCUS CL972569 864 bp DNA linear GSS 21-SEP-2004  
DEFINITION OsIFCC023161 Oryza sativa Expressed Sequence Library Oryza sativa (indica cultivar-group) genomic, genomic survey sequence.  
ACCESSION CL972569  
VERSION CL972569.1 GI:52399671  
KEYWORDS GSS.  
SOURCE Oryza sativa (indica cultivar-group)  
ORGANISM Oryza sativa (indica cultivar-group)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.  
1 (bases 1 to 864)  
Ma L., Wang, J., Chen, C., Liu, X., Su, N., Li, L., Wang, X., Cao, M., Jiao, Y., Sun, N., Zhang, X., Bao, J., Sun, D., Zhao, H., Yuan, L., Wang, G.K.S., Deng, X.W. and Wang, J.  
An analysis of transcriptional regulation of the rice genome and its comparison to Arabidopsis  
Unpublished (2004)  
Contact: Chen Chen  
Department of Bioinformatic  
Beijing Institute of Genomics  
Chinese Academy of Sciences, Beijing 101300, China  
Tel: 86-10-80481559  
Fax: 86-10-80488676  
Email: chenchen@genomics.org.cn  
Rice genomic sequence.  
Class: exon-trapped.  
Location/Qualifiers  
1..864  
/organism="Oryza sativa (indica cultivar-group)"  
/mol\_type="genomic DNA"

ORIGIN

Query Match 9.1%; Score 90.4; DB 10; Length 640;  
Best Local Similarity 68.9%; Pred. No. 1.8e-13;  
Matches 124; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

QY 531 CACATGCGAGGAGCAGCAGGAGGATGATGAGGTATAGGAGAGAGAGAGAGCGCGC 590  
DB 645 CGCAATGCTGAGAGGAGGAGGCGCAAGCTGATGAGGTACAGGAGAGAGAGAGAGGTG 704  
QY 591 CTATGACAGCAATTCCTGATGAGTCCAGAAAGCTTACGCTGAGCTTCGGCCATGGGT 650  
DB 705 CTACGAGAGCAATTCCTGATGAGTCCAGAAAGCTTACGCTGAGTTCGGCCATGGGT 764  
QY 651 CAACGCGCGCTTTGTCAAGGTACCCGAGCCATGCGCATCATCTCCAGTTCGCC 710  
DB 765 GAGAGTCTGCTTCGCCAAAGAGCTGA--TCAGGAAGCTGTGCGACCGCCATCCACCTA 821  
QY 711 CTATGATCTTGTAGTAACTTCACTCGGA 738  
DB 822 TGTGATCTTGTAGTAACTTCACTCGGA 849

RESULT 10  
CL925503  
LOCUS CL925503 640 bp DNA linear GSS 14-SEP-2004  
DEFINITION OA\_ABA0031L09.f OA\_ABA Oryza australiensis genomic clone  
ACCESSION CL925503  
VERSION CL925503.1 GI:52045241  
KEYWORDS GSS.  
SOURCE Oryza australiensis  
ORGANISM Oryza australiensis  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.  
1 (bases 1 to 640)  
Kim, H., Yu, Y., Stum, D., Yost, D., Rao, K., Luo, M., Jetty, R., Kudrna, D., Muller, C., Hatfield, J., Soderlund, C. and Wing, R.  
OMAP Project  
Unpublished (2004)  
Contact: Rod A. Wing  
Arizona Genomics Institute  
University of Arizona  
Forbes Building Room 303, Tucson, AZ 85721-0036, USA  
Tel: 520 626 9595  
Fax: 520 621 1259  
Email: rwing@genome.arizona.edu  
PCR Primers  
FORWARD: TAA TAC GAC TCA CTA TAG GG  
BACKWARD: CAC TCA TTA GGC ACC CCA  
Plate: 0031 row: L column: 09  
Seq primer: TAA TAC GAC TCA CTA TAG GG  
Class: BAC ends.  
Location/Qualifiers  
1..640  
/organism="Oryza australiensis"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:4532"  
/clone="OA\_ABA0031L09"  
/tissue\_type="young leaves"  
/lab\_host="DH10B T1 phage resistant"  
/clone\_lib="OA\_ABA"  
/note="Vector: pGIBAC1; Site\_1: HindIII; Site\_2: HindIII"

ORIGIN

Query Match 9.1%; Score 90.4; DB 10; Length 640;  
Best Local Similarity 68.9%; Pred. No. 1.8e-13;  
Matches 124; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

QY 531 CACATGCGAGGAGCAGCAGGAGGATGATGAGGTATAGGAGAGAGAGAGCGCGC 590  
DB 645 CGCAATGCTGAGAGGAGGAGGCGCAAGCTGATGAGGTACAGGAGAGAGAGAGGTG 704  
QY 591 CTATGACAGCAATTCCTGATGAGTCCAGAAAGCTTACGCTGAGCTTCGGCCATGGGT 650  
DB 705 CTACGAGAGCAATTCCTGATGAGTCCAGAAAGCTTACGCTGAGTTCGGCCATGGGT 764  
QY 651 CAACGCGCGCTTTGTCAAGGTACCCGAGCCATGCGCATCATCTCCAGTTCGCC 710  
DB 765 GAGAGTCTGCTTCGCCAAAGAGCTGA--TCAGGAAGCTGTGCGACCGCCATCCACCTA 821  
QY 711 CTATGATCTTGTAGTAACTTCACTCGGA 738  
DB 822 TGTGATCTTGTAGTAACTTCACTCGGA 849

Qy	540	GGAGAGCACCAGAGGTGATAGCGAGAGGAGAGCGCGCTATGACAA	599
Db	450	GGACCGGAGCGAAGGTGATCGGTCAAGAGAGAGGAGCGAGCGGTACGAGAA	509
Qy	600	GCAATCCGATACGAGTCCAGAAAGCTTACGCTGAGCTTCGGCCATGGGTCAACGGCCG	659
Db	510	GCAGATCCGGTACGCTCGCGAAGGCCATACGCGAGATTCGGCCGCGCGTGAAGGGCGC	569
Qy	660	CTTTGTCAAGGTACCCGAAGCCATGGCATCATCTCCAGCTTCGCCCTATGATGCC	719
Db	570	CTTCGCAAGGTGCCAGACGCGAGAGGGCGACGTCGCGCGCGCGTCTCCGCTGTC	629

RESULT 11	
CC879645/c	
LOCUS	
DEFINITION	CC879645 726 bp DNA linear GSS 29-JUL-2003 ZMVBb0214J20.r ZMVBb Zea mays genomic clone ZMVBb0214J20 3', genomic survey sequence.

ACCESSION	CC879645	
VERSION	CC879645.1	GI:33312386
KEYWORDS	GSS.	
SOURCE	Zea mays	
ORGANISM	Zea mays	
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.	

REFERENCE  
1 (bases 1 to 726)  
Yu, Y., Kim, H.R., Hatfield, J., Soderlund, C., Bharti, A.K., Messing, J.  
AUTHORS  
Andersson, R. and Wing, R.

**TITLE** Sequencing of the maize genome  
**JOURNAL** Unpublished (2003)  
**COMMENT** Contact: Rod Wing  
 Arizona Genomics Institute  
 University of Arizona  
 Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ  
 35721-0088, USA  
 Tel: 520 626 3967  
 Fax: 520 621 9288  
 Email: [rwing@genome.arizona.edu](mailto:rwing@genome.arizona.edu)

PCR Primers  
FORWARD: T7  
BACKWARD: M13r  
Plate: 0214 row: J column: 20  
Seq primer: M13r  
Class: BAC ends.

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FEATURES
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Location/Qualifiers
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/db_xref="taxon:4577"
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/lab_host="DH10B"
/clone_lib="ZMMBBB"
/note="Vector: pBelobAC11; Site 1: HindIII; Site 2: HindIII; Zea mays L. ssp. mays"

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ORIGIN

Query Match	9.1%	Score 90.4	DB 9	Length 726
Best Local Similarity	67.0%	Pred. No. 1.9e-13		
Matches 146	Conservative 0	Mismatches 66	Indels 6	Gaps 1

**Qy** 540 GGAGAGGCGAGGTGATGAGTATAGGAGAAGAGGGCGCTATGACAA 59  
||| | | | | | | | | | | | | | | | | | | | | | | | | |  
**Db** 224 GGACGGGAGGCCAAGGTGATCGGTAACAGGAAGCGGAGGAGCGCTACGAAA 16

Qy 600 GC<sup>AAATCCGATACGAGTCCAGAAAAAGCTTACGCTGAGCTTCGGCCATGGGTCAACGGCCG</sup> 65

Db 164 GCAGATTGGTACGCTCCGCAAGCCCTATGCAGAGATGCGGCCGCGGTCAAGGGCCG 10

Qy 660 CTTTGTCAAGGTACCGAAGCCATGGCATCG-----CCATCATCTCCAGCTTCGCCCTA 71

db 104 CTTGCCCAAGGTGCCCGACGGTGAGGTCCTCGCCACCGGGCGCGGCATGCTA 45

Qy	714	TGATCCTAGTAAACTTCACCTCGGATGGTTCGGTAAT	751
Db	44	CGAAC CAGGCCGTCTCAAGTCGGATGGTTCGGTTCAT	7

RESULT 12	
CL149066/c	
LOCUS	
DEFINITION	

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

## REFERENCE AUTHORS

TITLE	JOURNAL	PUBMED	COMMENT
-------	---------	--------	---------

**FEATURES**  
**source**

## ORIGIN

Query Match 8.9%; Score 89; DB 10; Length 736;  
Best Local Similarity 66.5%; Pred. No. 4.6e-13;  
Matches 147; Conservative 0; Mismatches 65; Indels

Qy 540 GGAGAGCAGCCGAGGTGATGAGGTATAGGAGAGAGAGAGGCGCGCTATGACAA 599

Db	388	GGACCGGGAGCGGAAGGTGATCGCATACAGGAGAAACGCGAAGAGGCGCTACGAGAA	329
Ov	600	GCAAAATCCGATACAGCTCCAGAAAAGCTTACGCTGAGCTTCGGCCATGGGTCAACCGGCGC	659

328 GCAGATTCGGTACGCTCCCGCAAGGCCTACGCAGAGATCGGCCCGCGTCAAGGCCG 269

Qy 660 CTTTGTCAAGGTACCCGAAG-----CCATGGCATCGGCATCATCTCGAGCTTCGCC 710

Db 268 GTTCGCCAAGGTGCCGACGTGACGCTCGGCGCCACCGCGCCGCCGCGGACGACGAG 209

QV 711 CTATGATCCTAGTAAACTTCACCTCGGATGGTTCGGTAAT 751





QY 585 GCGGCGCTATGACAGCAAAATCCGATACGAGTCCAGAAAAGCTTACGCTGAGCTTCGGCC 644  
 DB 578 ACCGAGGTACGAGAGCAGGTACCGGTACCGTCAAGGAAGGCGTACGCTGAGATGAAGCC 637  
 QY 645 ATGGGTCAACGGCGCGCTTTGTCAAGGTATCCCGAAGCCATGGCATGCC 692  
 DB 638 GAAGATAAAGGCGGCTTCGCAAGACGCCGGAGAGCCAGCCGCC 685

## RESULT 15

CK163737/c

LOCUS

CK163737 1061 bp mRNA linear EST 05-DEC-2003  
 FGAS016368 Triticum aestivum FGAS: Library 4 Gate 8 Triticum

aestivum cDNA, mRNA sequence.

ACCESSION

CK163737

VERSION

CK163737.1

GI:38994276

EST

Triticum aestivum (bread wheat)

Triticum aestivum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Poideae; Triticeae; Triticum.

1 (bases 1 to 1061)

Allard, F., Crosby, W.L., Danyluk, J., Budes, F., Frick, M., Gaudet, D.,

Genswein, B., Graf, R., Gulick, P., Hrycan, L.D., Laroche, A.,

Links, M.G., McCarthy, E.L., Monroy, A., Muzak, I., Nilsson, D.,

Penniket, C., Roach, J.L. and Sarhan, F.

Functional Genomics of Abiotic Stress In Wheat and Canola Crops

Unpublished (2003)

Contact: Mm L Crosby

Bioinformatics

University of Saskatchewan, Department of Computer Science

1C101 Engineering Building, 57 Campus Drive, Saskatoon,

Saskatchewan, S7N 5A9, Canada

Tel: 306 966 1769

Fax: 306 966 2033

Email: fgas.estcs.usask.ca

This sequence is the direct result of the Base calling software

Phred (default parameters). It is the raw base calls. To aid in the

identification of the high quality insert the software Lucy

(default parameters) has been run on this sequence. Lucy identified

the region [287,688].

Plate: L4B009 row: A column: 12.

Location/Qualifiers

1. .1061

/organism="Triticum aestivum"

/mol\_type="mRNA"

/db\_xref="taxon:4565"

/clone\_lib="Triticum aestivum FGAS: Library 4 Gate 8"

/note="Organ: Crown and leaf; Vector: pCMV.SPORT6;

Conditions for growth: Seeds were germinated in a

water-saturated mix (50% black earth and 50% proMix) in a

growth chamber for 7 days under an irradiance of 200 mmol

m-2 sec-1. The temperature was maintained at 20 degrees C

with a 15-hr photoperiod under a relative humidity of 70%.

After this period watering of plants was stopped. Four

time points were sampled during a two week period; the

first after wilting was observed and the last, two weeks

later, consisted of live crown and leaf tissue (leaf

tissue that was yellow was not included in sampled

material). First strand synthesis in this library was done

in the presence of methylated dCTP thereby protecting from

internal cleavage with NotI."

## ORIGIN

Query Match 7.8%; Score 77.2; DB 7; Length 1061;  
 Best Local Similarity 70.5%; Pred. No. 9.3e-10;  
 Matches 103; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

QY 532 ACAATCCAGGAGACGACGAGGTGATGAGGTATAGGAGAGAGAGAGAGAGCGCGC 591

DB 524 ACCGGGGAGGAGGAGGTGCGAGGCTGATCGGTACCGGGAGAGAGAGAGAGCGCGG 465

QY 592 TATGACAAAGCAAAATCCGATACGAGTCCAGAAAAGCTTACGCTGAGCTTCGGCCATGGGTC 651  
 DB 464 TTCGAGAAAGACCATCCGGTACCGGTACCGTCCAGGAAGGCTTACGCGCGCGCGCGTC 405  
 QY 652 AACGGCGCGCTTTGTCAAGGTATACCGCA 677  
 DB 404 AAGGCGCGCTTTCGCGCAAGCGCACCGA 379

Search completed: February 23, 2006, 14:49:49

Job time : 4767 secs

GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 23, 2006, 12:04:50 ; Search time 993 Seconds

(without alignments)  
8294.361 Million cell updates/sec

Title: US-10-723-947-75

Perfect score: 996

Sequence: 1 taactgcctctcttcttcc.....tagctactttgatgtgtaat 996

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA Main:

- 1: /cgn2\_6/ptodata/1/pubna/US07\_PUBCOMB.seq.\*
- 2: /cgn2\_6/ptodata/1/pubna/US08\_PUBCOMB.seq.\*
- 3: /cgn2\_6/ptodata/1/pubna/US09\_PUBCOMB.seq.\*
- 4: /cgn2\_6/ptodata/1/pubna/US09B\_PUBCOMB.seq.\*
- 5: /cgn2\_6/ptodata/1/pubna/US10A\_PUBCOMB.seq.\*
- 6: /cgn2\_6/ptodata/1/pubna/US10B\_PUBCOMB.seq.\*
- 7: /cgn2\_6/ptodata/1/pubna/US10C\_PUBCOMB.seq.\*
- 8: /cgn2\_6/ptodata/1/pubna/US10D\_PUBCOMB.seq.\*
- 9: /cgn2\_6/ptodata/1/pubna/US10E\_PUBCOMB.seq.\*
- 10: /cgn2\_6/ptodata/1/pubna/US11\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	996	100.0	996	8	US-10-723-947-75	Sequence 75, Appl
2	907.2	91.1	975	8	US-10-723-947-79	Sequence 79, Appl
3	561	56.3	7051	8	US-10-723-947-74	Sequence 74, Appl
4	553	55.5	2913	8	US-10-723-947-78	Sequence 78, Appl
5	455.2	45.7	642	8	US-10-723-947-91	Sequence 91, Appl
6	451.4	45.3	639	8	US-10-723-947-85	Sequence 85, Appl
7	449	45.1	639	8	US-10-723-947-88	Sequence 88, Appl
8	445	44.7	639	8	US-10-723-947-82	Sequence 82, Appl
9	320.8	32.2	3454	8	US-10-723-947-84	Sequence 84, Appl
10	320.8	32.2	5734	8	US-10-723-947-81	Sequence 81, Appl
11	251.4	25.2	2043	8	US-10-723-947-90	Sequence 90, Appl
12	247.6	24.9	1985	8	US-10-723-947-87	Sequence 87, Appl
13	92.8	9.3	864	7	US-10-437-963-83163	Sequence 83163, A
14	86	8.6	1413	7	US-10-437-963-82314	Sequence 82314, A
15	76.6	7.7	885	3	US-09-938-842A-265	Sequence 265, App
16	76.6	7.7	885	3	US-09-938-842A-265	Sequence 265, App
17	76.6	7.7	1075	7	US-10-425-114-22406	Sequence 22406, A
18	76.6	7.7	1120	7	US-10-412-699B-597	Sequence 597, App
19	76.6	7.7	1141	5	US-10-295-403-107	Sequence 107, App
20	75.4	7.6	577	7	US-10-260-238-390	Sequence 390, App
21	75.4	7.6	1768	7	US-10-437-963-40	Sequence 40, Appl
22	74.8	7.5	1002	7	US-10-260-238-403	Sequence 403, App
23	74.8	7.5	2717	7	US-10-437-963-30197	Sequence 30197, A

c	24	74.6	7.5	1320	7	US-10-437-963-25736	Sequence 25736, A
	25	73.8	7.4	589	8	US-10-425-115-111664	Sequence 111664, A
	26	73.6	7.4	1461	7	US-10-425-114-15481	Sequence 15481, A
	27	73.6	7.4	1521	8	US-10-425-115-111667	Sequence 111667, A
c	28	73	7.3	1139	7	US-10-437-963-101201	Sequence 101201, A
	29	72.2	7.2	388	9	US-10-487-901-1513	Sequence 1513, Ap
c	30	71.8	7.2	1297	3	US-09-770-445-17	Sequence 17, Appl
	31	71.8	7.2	1370	7	US-10-425-114-14597	Sequence 14597, A
	32	71.8	7.2	1404	7	US-10-425-114-13058	Sequence 13058, A
	33	71.6	7.2	1260	8	US-10-425-115-111666	Sequence 111666, A
	34	70	7.0	972	7	US-10-767-701-11858	Sequence 11858, A
	35	70	7.0	1132	7	US-10-425-114-25452	Sequence 25452, A
	36	70	7.0	1229	7	US-10-425-114-22309	Sequence 22309, A
	37	69.4	7.0	595	7	US-10-021-323-14874	Sequence 14874, A
c	38	68.4	6.9	533	7	US-10-021-323-16368	Sequence 16368, A
	39	68	6.8	1396	7	US-10-767-701-12421	Sequence 12421, A
	40	68	6.8	1436	8	US-10-425-115-50515	Sequence 50515, A
	41	67.6	6.8	901	8	US-10-425-115-34955	Sequence 34955, A
c	42	67.4	6.8	872	7	US-10-767-701-13864	Sequence 13864, A
	43	66.2	6.6	2065	7	US-10-437-963-15010	Sequence 15010, A
	44	65.8	6.6	742	8	US-10-425-115-157736	Sequence 157736, A
	45	65.8	6.6	801	7	US-10-424-599-1411	Sequence 1411, Ap

#### ALIGNMENTS

#### RESULT 1

US-10-723-947-75  
; Sequence 75, Application US/10723947  
; Publication No. US20040205848A1  
; GENERAL INFORMATION:  
; APPLICANT: Dubcovsky, Jorge  
; APPLICANT: Yan, Liuling  
; APPLICANT: Loukianov, Artem  
; TITLE OF INVENTION: GENES RESPONSIBLE FOR VERNALIZATION  
; TITLE OF INVENTION: REGULATION IN TEMPERATE GRASSES AND USES THEREOF  
; FILE REFERENCE: 514112000320  
; CURRENT APPLICATION NUMBER: US/10/723,947  
; PRIOR FILING DATE: 2003-11-26  
; PRIOR FILING DATE: 2003-04-11  
; NUMBER OF SEQ ID NOS: 159  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 75  
; TYPE: DNA  
; ORGANISM: Triticum monococcum  
US-10-723-947-75

Query Match	100.0%	Score	996	DB	8	Length	996
Best Local Similarity	100.0%	Pred. No.	1.4e-280				
Matches	996	Conservative	0	Mismatches	0	Indels	0
Gaps	0						
Qy	1	TAAC	TGCTCTTCTTCTTCTTCGACGCTCTCTCTCGGCTCTCTCCAGCAGCAGCAGCAGCA	60			
Db	1	TAAC	TGCTCTTCTTCTTCTTCGACGCTCTCTCTCGGCTCTCTCCAGCAGCAGCAGCA	60			
Qy	61	CACCAGAAAAA	CAAAACAAGCAAAACCTTGGAGCTAGCTAGCAGTATGTCCATGTCA	120			
Db	61	CACCAGAAAAA	CAAAACAAGCAAAACCTTGGAGCTAGCTAGCAGTATGTCCATGTCA	120			
Qy	121	TGCGTTTGTGCGGCGCA	CAACTGCGGCGCTCATGTCTGCGCCCATTCACCATCAT	180			
Db	121	TGCGTTTGTGCGGCGCA	CAACTGCGGCGCTCATGTCTGCGCCCATTCACCATCAT	180			
Qy	181	CATCACCATCATCAGGAGC	ACCAGCTGTGTAGTACCAAGTTCTTCGCCCATGGCAACAC	240			
Db	181	CATCACCATCATCAGGAGC	ACCAGCTGTGTAGTACCAAGTTCTTCGCCCATGGCAACAC	240			
Qy	241	CACCACCAACCA	CCATGGCTCGGAGCAGACTTACCAGTGCACCGCCGCGCAGAACATTC	300			
Db	241	CACCACCAACCA	CCATGGCTCGGAGCAGACTTACCAGTGCACCGCCGCGCAGAACATTC	300			



## RESULT 3

US-10-723-947-74  
; Sequence 74, Application US/10723947  
; Publication No. US20040205848A1  
; GENERAL INFORMATION:  
; APPLICANT: Dubcovsky, Jorge  
; APPLICANT: Loukoianov, Artem  
; TITLE OF INVENTION: GENES RESPONSIBLE FOR VERNALIZATION  
; FILE REFERENCE: 514112000320  
; CURRENT APPLICATION NUMBER: US/10/723,947  
; PRIOR FILING DATE: 2003-11-26  
; PRIOR APPLICATION NUMBER: US 10/412,137  
; NUMBER OF SEQ ID NOS: 159  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 74  
; LENGTH: 7051  
; TYPE: DNA  
; ORGANISM: Triticum monococcum  
US-10-723-947-74

Query Match 56.3%; Score 561; DB 8; Length 7051;  
Best Local Similarity 100.0%; Pred. No. 1e-152;  
Matches 561; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	436	GTGCCATTTACCGAGGTGCATTCCACCAACACTATTAGCAATGAAGCAATCATGACTATT	495
DB	4582	GTGCCATTTACCGAGGTGCATTCCACCAACACTATTAGCAATGAAGCAATCATGACTATT	4641
QY	496	GACACAGAGATGATGGTGGGGCTGCCCATTTATCCACAACTCCAGAGAGACGCGAAG	555
DB	4642	GACACAGAGATGATGGTGGGGCTGCCCATTTATCCCAATCCAGAGAGACGCGAAG	4701
QY	556	GTGATGAGGTATAGGGAGAAGAGAGGCGCGCTATGACAAAGCAAAATCCGATACCGAG	615
DB	4702	GTGATGAGGTATAGGGAGAAGAGAGGCGCGCTATGACAAAGCAAAATCCGATACCGAG	4761
QY	616	TCAGAAAAGCTTACGTGAGCTTGGCCATCATCTCCAGCTTCGCCCTATGATCCTAGTAAACTTCACCTC	735
DB	4762	TCAGAAAAGCTTACGTGAGCTTGGCCATCATCTCCAGCTTCGCCCTATGATCCTAGTAAACTTCACCTC	4821
QY	676	GAAGCCATGGCATCGCATCATCTCCAGCTTCGCCCTATGATCCTAGTAAACTTCACCTC	735
DB	4822	GAAGCCATGGCATCGCATCATCTCCAGCTTCGCCCTATGATCCTAGTAAACTTCACCTC	4881
QY	736	GGATGGTTCGGGTAAATTTATAGCAAGCCAGATAAAATGATAACATATTTCTCTGAT	795
DB	4882	GGATGGTTCGGGTAAATTTATAGCAAGCCAGATAAAATGATAACATATTTCTCTGAT	4941
QY	796	TGATCCACCCGTGAAGCAGTGTCTCTCAAGTAAATAAGTCGGTGTAGTATGATCGA	855
DB	4942	TGATCCACCCGTGAAGCAGTGTCTCTCAAGTAAATAAGTCGGTGTAGTATGATCGA	5001
QY	856	TTGGAGCCATTATGTGACTTGAATTTAAATGGTCAGAGATCAATCAAAACAAATG	915
DB	5002	TTGGAGCCATTATGTGACTTGAATTTAAATGGTCAGAGATCAATCAAAACAAATG	5061
QY	916	TATTTATTGAACAAAGTCTTGTATACGTGTTGATTTAAACATGTAATTTCAAGAGG	975
DB	5062	TATTTATTGAACAAAGTCTTGTATACGTGTTGATTTAAACATGTAATTTCAAGAGG	5121
QY	976	ATAGTACTTTGATGTGAAT	996
DB	5122	ATAGTACTTTGATGTGAAT	5142

## RESULT 4

US-10-723-947-78  
; Sequence 78, Application US/10723947  
; Publication No. US20040205848A1  
; GENERAL INFORMATION:  
; APPLICANT: Dubcovsky, Jorge  
; APPLICANT: Loukoianov, Artem  
; TITLE OF INVENTION: GENES RESPONSIBLE FOR VERNALIZATION  
; FILE REFERENCE: 514112000320  
; CURRENT APPLICATION NUMBER: US/10/723,947  
; PRIOR FILING DATE: 2003-11-26  
; PRIOR APPLICATION NUMBER: US 10/412,137  
; NUMBER OF SEQ ID NOS: 159  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 78  
; LENGTH: 2913  
; TYPE: DNA  
; ORGANISM: Triticum dicoccoides  
US-10-723-947-78

APPLICANT: Dubcovsky, Jorge  
APPLICANT: Yan, Liuling  
APPLICANT: Loukoianov, Artem  
TITLE OF INVENTION: GENES RESPONSIBLE FOR VERNALIZATION  
FILE REFERENCE: 514112000320  
CURRENT APPLICATION NUMBER: US/10/723,947  
PRIOR FILING DATE: 2003-11-26  
PRIOR APPLICATION NUMBER: US 10/412,137  
NUMBER OF SEQ ID NOS: 159  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 78  
LENGTH: 2913  
TYPE: DNA  
ORGANISM: Triticum dicoccoides  
US-10-723-947-78

Query Match 55.5%; Score 553; DB 8; Length 2913;  
Best Local Similarity 99.1%; Pred. No. 1.4e-150;  
Matches 556; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY	436	GTGCCATTTACCGAGGTGCATTCCACCAACACTATTAGCAATGAAGCAATCATGACTATT	495
DB	2133	GTGCCATTTACCGAGGTGCATTCCACCAACACTATTAGCAATGAAGCAATCATGACTATT	2192
QY	496	GACACAGAGATGATGGTGGGGCTGCCCATTTATCCCAATCCAGAGAGACGCGAAG	555
DB	2193	GACACAGAGATGATGGTGGGGCTGCCCATTTATCCCAATCCAGAGAGACGCGAAG	2252
QY	556	GTGATGAGGTATAGGGAGAAGAGAGGCGCGCTATGACAAAGCAAAATCCGATACCGAG	615
DB	2253	GTGATGAGGTATAGGGAGAAGAGAGGCGCGCTATGACAAAGCAAAATCCGATACCGAG	2312
QY	616	TCAGAAAAGCTTACGTGAGCTTGGCCATCATCTCCAGCTTCGCCCTATGATCCTAGTAAACTTCACCTC	735
DB	2313	TCAGAAAAGCTTACGTGAGCTTGGCCATCATCTCCAGCTTCGCCCTATGATCCTAGTAAACTTCACCTC	2372
QY	676	GAAGCCATGGCATCGCATCATCTCCAGCTTCGCCCTATGATCCTAGTAAACTTCACCTC	735
DB	2373	GAAGCCATGGCATCGCATCATCTCCAGCTTCGCCCTATGATCCTAGTAAACTTCACCTC	2432
QY	736	GGATGGTTCGGGTAAATTTATAGCAAGCCAGATAAAATGATAACATATTTCTCTGAT	795
DB	2433	GGATGGTTCGGGTAAATTTATAGCAAGCCAGATAAAATGATAACATATTTCTCTGAT	2492
QY	796	TGATCCACCCGTGAAGCAGTGTCTCTCAAGTAAATAAGTCGGTGTAGTATGATCGA	855
DB	2493	TGATCCACCCGTGAAGCAGTGTCTCTCAAGTAAATAAGTCGGTGTAGTATGATCGA	2552
QY	856	TTGGAGCCATTATGTGACTTGAATTTAAATGGTCAGAGATCAATCAAAACAAATG	915
DB	2553	TTGGAGCCATTATGTGACTTGAATTTAAATGGTCAGAGATCAATCAAAACAAATG	2612
QY	916	TATTTATTGAACAAAGTCTTGTATACGTGTTGATTTAAACATGTAATTTCAAGAGG	975
DB	2613	TATTTATTGAACAAAGTCTTGTATACGTGTTGATTTAAACATGTAATTTCAAGAGG	2672
QY	976	ATAGTACTTTGATGTGAAT	996
DB	2673	ATAGTACTTTGATGTGAAT	2693

## RESULT 5

US-10-723-947-91  
; Sequence 91, Application US/10723947  
; Publication No. US20040205848A1  
; GENERAL INFORMATION:  
; APPLICANT: Dubcovsky, Jorge  
; APPLICANT: Loukoianov, Artem  
; TITLE OF INVENTION: GENES RESPONSIBLE FOR VERNALIZATION  
; FILE REFERENCE: 514112000320  
; CURRENT APPLICATION NUMBER: US/10/723,947  
; PRIOR FILING DATE: 2003-11-26  
; PRIOR APPLICATION NUMBER: US 10/412,137  
; NUMBER OF SEQ ID NOS: 159  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 91  
; LENGTH: 2913  
; TYPE: DNA  
; ORGANISM: Triticum dicoccoides  
US-10-723-947-91

FILE REFERENCE: 514112000320  
; CURRENT APPLICATION NUMBER: US/10/723,947  
; CURRENT FILING DATE: 2003-11-26  
; PRIOR APPLICATION NUMBER: US 10/412,137  
; PRIOR FILING DATE: 2003-04-11  
; NUMBER OF SEQ ID NOS: 159  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 91  
; LENGTH: 642  
; TYPE: DNA  
; ORGANISM: Hordeum vulgare  
US-10-723-947-91

Query Match 45.7%; Score 455.2; DB 8; Length 642;  
Best Local Similarity 83.0%; Pred. No. 2.9e-122;  
Matches 533; Conservative 0; Mismatches 103; Indels 6; Gaps 1;  
QY 109 ATGTCATCTCATCGGTTTGTGCGCGCCCAACAACTGCCCGGCTCATGCTCTCGCC 168  
DB 1 ATGTCATGCGATGCGGTTTGTGCGCGCCCAACAACTGCCCGGCTCATGCTCTCGCC 60  
QY 169 ATTACCATCATCATCACCATCATCAGGAGCACCAGCTGTGTAGTACCACTTCTTCGCC 228  
DB 61 GTTCTTCTCATCATCACCATCATCAGGAGCACCAGCTGTGTAGTACCACTTCTTCGCC 120  
QY 229 CATGCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCA 288  
DB 121 CAAGGTCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCA 180  
QY 289 CCAGCACTTCCAGCACTTCCAGCACTTCCAGCACTTCCAGCACTTCCAGCACTTCCAGCA 348  
DB 181 CCGGCAATTTGCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCA 240  
QY 349 GGGAAACAGCAGCAGGCTCAACGCTGAGGTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 408  
DB 241 GTGATAGCAGCAGGCTCAACAGAGGTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 300  
QY 409 GTGAGCCACCGG-----CAAGAGCCCACTGTCGCCATTTTACGGAGTGCATTCACC 462  
DB 301 CTGAGCCACCGGCG 360  
QY 463 AACCTATTAGCAATCAGCACTATGACTATTGACAGAGATGATGGTGGGCGCTGCC 522  
DB 361 AACCTATTAGCAACGCAACGATCATGACTATTGATACAGATGATGGTGGGCGCTGCC 420  
QY 523 CATTATCCCAATTCAGAGAGCAGCGAAGGTGATGAGGTATAGGAGAGAGGAGAG 582  
DB 421 TATAGTCCCAACGATCAG 480  
QY 583 AGCGCGGCTATGACAAGCAATCCGATACGAGTCCAGAAAGCTTACGCTGAGCTTCGG 642  
DB 481 AAGCGGCTATGACAAGCAATCCGATACGAGTCCAGAAAGCTTACGCTGAGCTTCAGG 540  
QY 643 CCATGGGTCAACGGCGCTTTGTCAAGGTACCGAGCCATGGCATCGCATCATCTCCA 702  
DB 541 CCACGGGTCAACGGCGCTTTGTCAAGGTACCGAGTACCGAGCGCTGCATCATCCCCCA 600  
QY 703 GCTTCGCCCTATGATCTAGTAACTTACCTCGGATGGTTC 744  
DB 601 GCTTCGCCCTATGATCTAGTAACTTACCTCGGATGGTTC 642

RESULT 6  
US-10-723-947-85  
; Sequence 85, Application US/10723947  
; Publication No. US20040205848A1  
; GENERAL INFORMATION:  
; APPLICANT: Dubcovsky, Jorge  
; APPLICANT: Yan, Liuling  
; APPLICANT: Loukoianov, Artem  
; TITLE OF INVENTION: GENES RESPONSIBLE FOR VERNALIZATION  
; TITLE OF INVENTION: REGULATION IN TEMPERATE GRASSES AND USES THEREOF  
; FILE REFERENCE: 514112000320

; CURRENT APPLICATION NUMBER: US/10/723,947  
; CURRENT FILING DATE: 2003-11-26  
; PRIOR APPLICATION NUMBER: US 10/412,137  
; PRIOR FILING DATE: 2003-04-11  
; NUMBER OF SEQ ID NOS: 159  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 85  
; LENGTH: 639  
; TYPE: DNA  
; ORGANISM: Triticum dicoccoides  
US-10-723-947-85

Query Match 45.3%; Score 451.4; DB 8; Length 639;  
Best Local Similarity 83.6%; Pred. No. 3.7e-121;  
Matches 541; Conservative 0; Mismatches 91; Indels 15; Gaps 2;  
QY 109 ATGTCATCTCATCGGTTTGTGCGCGCCCAACAACTGCCCGGCTCATGCTCTCGCC 168  
DB 1 ATGTCATCTCATCGGTTTGTGCGCGCCCAACAACTGCCCGGCTCATGCTCTCGCC 60  
QY 169 ATTACCATCATCATCACCATCATCAGGAGCACCAGCTGTGTAGTACCACTTCTTCGCC 228  
DB 61 GTTCT-----TCAGCATCAGGAACAACACACCGGCTGCGAGTACCACTTCTTCACC 111  
QY 229 CATGCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCA 288  
DB 112 CAAGGTCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCA 171  
QY 289 CCAGCACTTCCAGCACTTCCAGCACTTCCAGCACTTCCAGCACTTCCAGCACTTCCAGCA 348  
DB 172 TCAGCAATTTGCCAATCTGCACTGATCATGATCATGATCATGATCATGATCATGATCATG 231  
QY 349 GGGAAACAGCAGCAGGCTCAACGCTGAGGTGGCGCGCGCGCGCGCGCGCGCGCGCGCG 408  
DB 232 GGGAAACAGCAGCAGGCTCAACGCTGAGGTGGCGCGCGCGCGCGCGCGCGCGCGCGCG 291  
QY 409 GTGAGCCACCGG-----CAAGAGCCCACTGTCGCCATTTTACGGAGTGCATTCACC 462  
DB 292 CTGAGCCACCGGCG 351  
QY 463 AACCTATTAGCAATCAGCACTATGACTATTGACAGAGATGATGGTGGGCGCTGCC 522  
DB 352 AGCACTATTAGCAATGCAACGATCATGACTATTGATACAGAGATGATGGTGGGCGCTGCC 411  
QY 523 CATTATCCCAATTCAGAGAGCAGCGAAGGTGATGAGGTATAGGAGAGAGGAGAG 582  
DB 412 CATAATCTGACGATGACGAG 471  
QY 583 AGCGCGGCTATGACAAGCAATCCGATACGAGTCCAGAAAGCTTACGCTGAGCTTCGG 642  
DB 472 AGCGGCTGATGACAAGCAATCCGATACGAGTCCAGAAAGCTTACGCTGAGCTTCAGG 531  
QY 643 CCATGGGTCAACGGCGCTTTGTCAAGGTACCGAGCCATGGCATCGCATCATCTCCA 702  
DB 532 CCACGGGTCAACGGCGCTTTGTCAAGGTACCGAGCCGCTGCATCGCTGCATCCCCCA 591  
QY 703 GCTTCGCCCTATGATCTAGTAACTTACCTCGGATGGTTC 749  
DB 592 GCTTCGCCCTATGATCTAGTAACTTACCTCGGATGGTTC 638

RESULT 7  
US-10-723-947-88  
; Sequence 88, Application US/10723947  
; Publication No. US20040205848A1  
; GENERAL INFORMATION:  
; APPLICANT: Dubcovsky, Jorge  
; APPLICANT: Yan, Liuling  
; APPLICANT: Loukoianov, Artem  
; TITLE OF INVENTION: GENES RESPONSIBLE FOR VERNALIZATION  
; TITLE OF INVENTION: REGULATION IN TEMPERATE GRASSES AND USES THEREOF  
; FILE REFERENCE: 514112000320  
; CURRENT APPLICATION NUMBER: US/10/723,947

Query Match	44.7%	Score 445	DB 8	Length 639
Best Local Similarity	83.0%	Pred. No. 2.8e-119		
Matches 537	Conservative 0	Mismatches 95	Indels 15	Gaps 2
Qy	109	ATGTCATGTCATGCGGTTTGTGCGGCGCCAAACAACCTGCCCGCCCTCATGCTTCGCCC	168	
Db	1	ATGTCATGTCATGCGGTTTGTGCGGCGCAAGCGACTGCCCGCACCATGATGTCGCCC	60	
Qy	169	ATTCCACCATCATCATCACCATCATCAGGAGCACCGCTGTGTGAGTACCAAGTCTTCGCCC	228	
Db	61	GT-----TCTTCAGCATCAGGAACAACATGGCTGCGGAGTACCAAGTCTTCACCC	111	
Qy	229	CATGGCAACCAACCAACCAACCATGGCTCGCGCAGCAGACTACCCAGTCCCAACCGCGC	288	
Db	112	CAAGGCCAACCAACCAACCAACCGCGCGCGCGGCGGACTACCCACCGCCACCGCACCG	171	
Qy	289	CCAGACAATTCGACCAACCGCAGAAACATGACACAGACCAATTTATGAAACAGCAGCGCA	348	
Db	172	TCGGCCAAATGGCACCACTGCAGATCATGACCAACACCGTTTTCATGAAACAGCAGCTCA	231	
Qy	349	GGGAAACAGCAGCAGGCTCAGCTGGAGGTGGCGCAGCGCGCCAAACATGGCTCACCTTA	408	
Db	232	GGGAAACAGCAGCAGACTCAACCTGGAGGTAGATGCAGCGCGCCAAACATGGCTCACCTG	291	
Qy	409	GTGACGCCACCGG-----CAAGAGCCCAACATCGTGCCATTTTCAGGAGGTGCATTCACC	462	
Db	292	CTGACGCCACCGGCAACCGCCCAAGAACACCATCGTGCCATTTCTCGGGGCTGCATTCACC	351	
Qy	463	AACACTATTAGCAATGAGCAATCATGACTATTTCACACAGAGATGATGGTGGGCGCTGCC	522	
Db	352	AGCACTATTAGCAATGCAACAAATCATGACTATTGATACAGAGATGATGGTGGGCGCTGCC	411	
Qy	523	CATTATCCCAATGCAGAGAGACAGCAGCAAGTGTATGAGGTATAGGGAAGAAGGAAG	582	
Db	412	CATAATCTGACGATGCAGGAGAGAGGCGAAGGTGATGAGGTACAGGGAAGAAGGAAG	471	
Qy	583	AGCGCGGCTATGACAAGCAAAATTCGATACGAGTCCAGAAAAGCTTACGCTGAGCTTCGG	642	
Db	472	AGCGCGTGTATGACAAGCAAAATCCGCTACGAGTCCAGAAAAGCTTACGCGCAGCTCAGG	531	
Qy	643	CCATGGGTCAACGGCGCTTTGTCAAGGTACCCGAGCCATGGCATCGCCCATCATCTCCA	702	
Db	532	CCAGGGTCATGGCTGCTTTGTCAAGGTACCAAGACCGCTGCATGTCGTCAACCCCA	591	
Qy	703	GCTTCGCCCTATGATCCTAGTAAACTTCACCTCGGATGGTTCGGTA	749	
Db	592	GCTTCGCCCTATGATCCTAGTAAACTTCACCTCGGATGGTTCAGTA	638	

RESULT 9  
US-10-723-947-84  
; Sequence 84, Application US/10723947  
; Publication No. US20040205848A1.  
; GENERAL INFORMATION:  
; APPLICANT: Dubcovsky, Jorge  
; APPLICANT: Yan, Liuling  
; APPLICANT: Loukoianov, Artem  
; TITLE OF INVENTION: GENES RESPONSIBLE FOR VERNALIZATION  
; TITLE OF INVENTION: REGULATION IN TEMPERATE GRASSES AND USES THEREOF  
; FILE REFERENCE: 514112000320  
; CURRENT APPLICATION NUMBER: US/10/723,947  
; CURRENT FILING DATE: 2003-11-26  
; PRIOR APPLICATION NUMBER: US 10/412,137

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; -PRIOR FILING DATE: 2003-04-11
; NUMBER OF SEQ ID NOS: 159
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 84
; LENGTH: 3454
; TYPE: DNA
; ORGANISM: Triticum dicoccoides
US-10-723-947-84

Query Match      32.2%; Score 320.8; DB 8; Length 3454;
Best Local Similarity 77.4%; Pred. No. 1.7e-82;
Matches 432; Conservative 0; Mismatches 62; Indels 64; Gaps 1;

Qy 436 GTGCCATTTCACGGAGTGCATTCCACCAACACTATTAGCAATGAAGCAATCATGACTATT 495
Db 2645 GTGCCATTTCGCGGGGTGCATTCCACGACACTATTAGCAATGCAACGATCATGACTATT 2704

Qy 496 GACACAGAGATGATGGTGGGGCTTCGCCATTATCCCACTATGCCAGAGAGAGAGCGAAG 555
Db 2705 GATACAGAGATGATGGTGGGGCTTCGCCATAATCTGACGATGCGAGGAGAGAGGGCGAAG 2764

Qy 556 GTGATAGGTATAGGGAGAGAGAGGAGCGGGCTTATGACAAGCAAAATCCGATACGAG 615
Db 2765 GTGATAGGTATAGGGAGAGAGAGGAGCGGGTCTATGACAAGCAAAATCCGCTATGAG 2824

Qy 616 TCCAGAAAAGCTTACGCTGAGCTTCGGCCATGGGTCAACGGCGCCTTTGTCAAGGTACCC 675
Db 2825 TCCAGAAAAGCTTACGCGCGAGCTCAGGCCACGGGTCAATGGCGCTTTGTCAAGGTACCA 2884

Qy 676 GAAGCCATGCGATCGCCATCATCTCCAGCTTCGCCCTATGATCTAGTAAACTTCACCTC 735
Db 2885 GAAGCCCTGCATCGCTGCATCACCCTCAGCTTCGCCCTATGATCTAGTAAACTTCACCTC 2944

Qy 736 GGATGGTTCGGGTAATTTATAGCAACAAGCCAGATAAAATGATAACATATTTCTCTGAT 795
Db 2945 GGATGGTTCGGGTAGTTT----- 2962

Qy 796 TGATCCACCCTGGAAGCAGTTGTTCTCAAAGTAAAAATAAGTCGGTTAGTGTGATCGA 855
Db 2963 -----TTTCATCAAGTAAAAATAAGTTGGTTATTGTTTGACCGA 3000

Qy 856 TTGGAGCCATATGTTGACTTGACTATTATAATGGTCAGCAGATCAATCAACAAAATG 915-
Db 3001 TGGGAGAGTTATGTGATTGACTATTTCAAAAGGTCAGCAGACCAATCAAAAGAAAATG 3060

Qy 916 TATTATTGAAACAAGTCTGTTATATACGTGTTGATTTAAACATGTAATTTCAAGAGG 975
Db 3061 TATTGTTGAACAAGTATTGTTATGCTTTATGTTAATTTAAGCAUGTAGTTTGAGGAGG 3120

Qy 976 ATAGCTACTTTGATGCT 993
Db 3121 CTAGCTACTTTAGATGCT 3138

RESULT 10
US-10-723-947-81
; Sequence 81, Application US/10723947
; Publication No. US20040205848A1
; GENERAL INFORMATION:
; APPLICANT: Dubcovsky, Jorge
; APPLICANT: Yan, Liuling
; APPLICANT: Loukolanov, Artem
; TITLE OF INVENTION: GENES RESPONSIBLE FOR VERNALIZATION
; TITLE OF INVENTION: REGULATION IN TEMPERATE GRASSES AND USES THEREOF
; FILE REFERENCE: 514112000320
; CURRENT APPLICATION NUMBER: US/10/723,947
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US 10/412,137
; PRIOR FILING DATE: 2003-04-11
; NUMBER OF SEQ ID NOS: 159
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 81
; LENGTH: 5734

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; LOCATION: 1242, 1243, 1244, 1245, 1246, 1247, 1248, 1249, 1250, 1251,
; LOCATION: 1252, 1253, 1254, 1255, 1256, 1257, 1258, 1259, 1260, 1261,
; LOCATION: 1262, 1263, 1264, 1265, 1294, 1300, 1313, 1326, 1340
; OTHER INFORMATION: n = A,T,C or G
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1359, 1385
; OTHER INFORMATION: n = A,T,C or G
US-10-723-947-90

Query Match      25.2%; Score 251.4; DB 8; Length 2043;
Best Local Similarity 88.3%; Pred. No. 2.7e-62;
Matches 273; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

Qy 436 GTGCCATTTCAGGAGGTGCATTACCAACACTATTAGCAATGAAGCAATCATGACTATT 495
Db 1735 GTGCCATTCCGCGGAGTGCATTACCAACACTATTAGCAACGCACGATCATGACTATT 1794
Qy 496 GACACAGAGATGATGGTGGGCGCTGCCCATTTATCCCAATGCAGGAGAGAGCGGAAG 555
Db 1795 GATACAGAGATGATGGCGGGACTGCCTATAGTCCACGATGCAGGAAGAGAGCAAG 1854
Qy 556 GTGATAGGTTATAGGAGAAAGAGAGAGGGCGGCTATGACAGCAAAATCCGATACGAG 615
Db 1855 GTGATAGGTTACAGGAGAAAGAGAGAGGGCGGCTATGACAGCAAAATCCGCTACGAG 1914
Qy 616 TCCAGAAAAGCTTACGCTGAGCTTCGGCCATGGGTCAACGCCCGCTTTGTCAAGGTACCC 675
Db 1915 TCCAGAAAAGCTTACGCGGAGCTTAGGCCACCGGTCAACGCCCGCTTTGTCAAGGTACCT 1974
Qy 676 GAAGCCATGGCATCGCCATCATCTCCAGCTTCGCGCCTATGATCCTAGTAAACTTCACCTC 735
Db 1975 GAAGCCGCTGGTCACCATCACCCACAGCTTCGCCCCCATGATCCTAGTGAATTCACCTC 2034
Qy 736 GGATGGTTC 744
Db 2035 GGATGGTTC 2043

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```

RESULT 12
US-10-723-947-87
; Sequence 87, Application US/10723947
; Publication No. US20040205848A1
; GENERAL INFORMATION:
; APPLICANT: Dubcovsky, Jorge
; APPLICANT: Yan, Liuling
; APPLICANT: Loukoianov, Artem
; TITLE OF INVENTION: GENES RESPONSIBLE FOR VERNALIZATION
; TITLE OF INVENTION: REGULATION IN TEMPERATE GRASSES AND USES THEREOF
; FILE REFERENCE: 514112000320
; CURRENT APPLICATION NUMBER: US/10723,947
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US 10/412,137
; PRIOR FILING DATE: 2003-04-11
; NUMBER OF SEQ ID NOS: 159
; SOFTWARE: fastseq for Windows Version 4.0
; SEQ ID NO 87
; LENGTH: 1985
; TYPE: DNA
; ORGANISM: Hordeum vulgare
US-10-723-947-87

Query Match          24.9%; Score 247.6; DB 8; Length 1985;
Best Local Similarity 81.0%; Pred. No. 3.4e-61;
Matches 342; Conservative 0; Mismatches 64; Indels 16; Gaps 4;

QY      4   CTGCCTCTTCTTCTTCCTCGACGCTCTCTCTCCTCGGCTCCTCCACGACGACACACACAC 63
DB      238 CTGCTCTTCTTCTTCTCTCGACATCTCTCTTCCAG-----CACCAGACACACACGAA 291

QY      64   CAGAAAAAACAACAAGCAACAAACCTTGGAGCTAGCTAGCAGTAGTGTCCATGTCTATGC 123
DB      292 ACAAAACAACCTAGCAACAACAACAAACGTTGGAGTTAGCT-GCAGTAGTGTCCATGTCTATGT 350

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QY	124	GGTTTGTGCGCGCGCAACAACTGCGCCCGCGCTCTATGFTCTCGCCCAATTCACCATCATCAT	18
DB	351	GGTTTGTGCGCGCGCGCAACTGCGCGCGTACCAATGATGTGCGCCGTTCTTCTTTCATCAT	410
QY	184	CACCATCATCAGGAGCACCAGCTGTGTGATGACCAAGTTCTTTGCGCCATGGCAACACCAC	243
DB	411	CACCATCATCAGGAACACCCACTGCACGAGTACCAGTTCTTTGCGCCAAAG-----TCAC	464
QY	244	CACCACCACTATGGCTCGGCAGCAGACTTACCAGTGCACCG---CCGCCAGACAACTTC	300
DB	465	CACCACCACTACAGCGCGGAGCGGACTACCCACCAACCGCCACCGCCAGACAAATTC	524
QY	301	GACCACCGCAGAAACATGACACAGACCAATTTTCATGAAACAGCAGCGGCAAGGAAACAGCAGC	360
DB	525	CACCACCAACAGATCATGCAACACCGCGTTTCATGAAACAGCAGCTCCAGAGAAACAGCACC	584
QY	361	AGGCTCAGCTGGAGGTGGGCGCAGGCGGCCAAACATATGGCTTCACCTAGTCAGGCCACCG	420
DB	585	AGGCTCAGCGGAGGTGGGCGCAGGCGGCCAAACATATGGCTTCACCTAGTCAGGCCACCG	644
QY	421	GC 422	
DB	645	GC 646	

RESULT 13  
 US-10-437-963-83163  
 ; Sequence 83163, Application US/10437963  
 ; Publication No. US20040123343A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: La Rosa, Thomas J.  
 ; APPLICANT: Kovalic, David K.  
 ; APPLICANT: Zhou, Yihua  
 ; APPLICANT: Cao, Yongwei  
 ; APPLICANT: Wu, Wei  
 ; APPLICANT: Boukharov, Andrey A.  
 ; APPLICANT: Barbazuk, Brad  
 ; APPLICANT: Li, Ping  
 ; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated  
 ; FILE REFERENCE: 38-21(53221)B  
 ; CURRENT APPLICATION NUMBER: US/10/437,963  
 ; CURRENT FILING DATE: 2003-05-14  
 ; NUMBER OF SEQ ID NOS: 204966  
 ; SEQ ID NO 83163  
 ; LENGTH: 864  
 ; TYPE: DNA  
 ; ORGANISM: Oryza sativa  
 ; FEATURE:  
 ; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_82521C.1  
 US-10-437-963-83163

QY	531	CACAATCCAGGAGACACCGAAGGTGATCAGGTATAGGAGAGAGAGAGAGCGCGC	590
DB	645	CGCAATGGTGGAGGGAGGCGCAAGCTGTATGAGTACAGGAGAGAGAGAGAGAGGTG	704
QY	591	CTATGACAAGCAATCCGATACGAGTCCAGAAAAAGCTTACGCTGAGCTTCGGCCATGGGT	650
DB	705	CTACGAGAGCAATTCGGTACGGTCCAGAAAGCCATATGCCGAGATGAGGCCCGAGT	764
QY	651	CAACGGCGCTTTGTCAAGGTACCCGAAGCGCATCGGCATTCGCGCATCATCTCCAGTTTCGCC	710
DB	765	GAGAGGTGCGTTTCGCCAAAGAACCTGA---TCAGAAAGCTGTCGCAACCGCATCCACCTA	821
QY	711	CTATGATCCTAGTAAACTTCACCTCGGA	738
DB	822	TGTCGATCTCTAGTAGGCTTCGAGCTTGA	849

Query Match 9.3%; Score 92.8; DB 7; Length 864;  
 Best Local Similarity 68.8%; Pred. No. 4.9e-16;  
 Matches 143; Conservative 0; Mismatches 62; Indels 3; Gaps 1

RESULT 14  
US-10-437-963-82314  
; Sequence 82314, Application US/10437963  
; Publication No. US20040123343A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Wu, Wei  
; APPLICANT: Boukharov, Andrey A.  
; APPLICANT: Barbazuk, Brad  
; APPLICANT: Li, Ping  
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53221)B  
; CURRENT APPLICATION NUMBER: US/10/437,963  
; CURRENT FILING DATE: 2003-05-14  
; NUMBER OF SEQ ID NOS: 204966  
; SEQ ID NO 82314  
; LENGTH: 1413  
; TYPE: DNA  
; ORGANISM: Oryza sativa  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT MRT4530\_81756C.1  
US-10-437-963-82314

Query Match 8.6%; Score 86; DB 7; Length 1413;  
Best Local Similarity 75.4%; Pred. No. 6.2e-14;  
Matches 107; Conservative 0; Mismatches 35; Indels 0; Gaps 0;  
QY 540 GGAGAGAGCAGCGAGGTGATAGGTATAGGGAGAGAGAGAGCGCGCTATGACAA 599  
DB 702 GCACCGGAGGCGAGGTGCGGTACAGGAGAGAGAGAGCGGCGATACGAGAA 761  
QY 600 GCAATCCGATACGATCCAGAAAGCTTACGCTGAGCTTCGGCCATGGGTCAACGCGCG 659  
DB 762 GCAGATCCGCTACGCTCGCGAAGGCTACGCCGAGATCGCGCGCGCGTGAAGGCGG 821  
QY 660 CTTTGTCAAGGTACCCGAGGCC 681  
DB 822 CTTGCCAAGGTGCGCGACGGC 843

RESULT 15  
US-09-938-842A-265  
; Sequence 265, Application US/09938842A  
; Patent No. US20020160378A1  
; GENERAL INFORMATION:  
; APPLICANT: Harper, Jeff  
; APPLICANT: Kreps, Joel  
; APPLICANT: Wang, Xun  
; APPLICANT: Zhu, Tong  
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING  
; TITLE OF INVENTION: SAME, AND METHODS OF USE  
; FILE REFERENCE: SCRIPI300-3  
; CURRENT APPLICATION NUMBER: US/09/938,842A  
; CURRENT FILING DATE: 2001-08-24  
; PRIOR APPLICATION NUMBER: US 60/227,866  
; PRIOR FILING DATE: 2000-08-24  
; PRIOR APPLICATION NUMBER: US 60/264,647  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: US 60/300,111  
; PRIOR FILING DATE: 2001-06-22  
; NUMBER OF SEQ ID NOS: 5379  
; SEQ ID NO 265  
; LENGTH: 885  
; TYPE: DNA  
; ORGANISM: Arabidopsis thaliana  
US-09-938-842A-265

Query Match 7.7%; Score 76.6; DB 3; Length 885;

Best Local Similarity 62.1%; Pred. No. 2.8e-11;  
Matches 121; Conservative 0; Mismatches 74; Indels 0; Gaps 0;  
QY 488 TGACTATTGACACAGAGATGATGGTGGGCGCTGCCCATTTATCCCAATGCGAGGAGAG 547  
DB 629 TGACGCGGAGATGACGAACACCGGAGACCCAGCTGTGCAGTTATCCCGCGGAGAGGG 688  
QY 548 CAGCGAAGGTGATAGGTATAGGGAGAGAGAGAGCGCGCTATGACAAAGCAATCC 607  
DB 689 AAGCAAGGCTTTTGGGTATAGAGAGAGAGAGAGAGTTCGAAATTTTGAGAGAGCGATT 748  
QY 608 GATACAGTCCAGAAAAGCTTACGCTGAGCTTCGGCCATGGGTCAACGCGCGCTTTGTCA 667  
DB 749 GGTATGCGCTCGCGTAAAGCTTACGCTGAGATGAGCGCGAGAAATCAAAGGACGCTTTTGTCA 808  
QY 668 AGGTACCCGAGGCCA 682  
DB 809 AGAGAACAGATTCCA 823

Search completed: February 23, 2006, 14:12:45  
Job time : 995 secs

C	1	43.8	4.4	162013	12	US-11-150-888-30	Sequence 30, Appl
	2	43.6	4.4	200628	12	US-11-121-086-62	Sequence 62, Appl
	3	41.4	4.2	908	12	US-11-128-061-549	Sequence 549, App
	4	41.4	4.2	908	12	US-11-128-049-549	Sequence 549, App
	5	41.2	4.1	17263	8	US-10-995-561-13411	Sequence 13411, A
	6	41.2	4.1	93112	8	US-10-995-561-13234	Sequence 13234, A
C	7	41.2	4.1	105550	8	US-10-995-561-13235	Sequence 13235, A
	8	41	4.1	15544	12	US-11-010-239-112	Sequence 112, App
	9	40.8	4.1	7402	8	US-10-750-185-27313	Sequence 27313, A
	10	40.8	4.1	7402	8	US-10-750-623-27313	Sequence 27313, A
	11	40	4.0	565	6	US-09-925-065A-809991	Sequence 809991, A
C	12	40	4.0	659	6	US-09-925-065A-26496	Sequence 26496, A
C	13	39.8	4.0	628	6	US-09-925-065A-640012	Sequence 640012, A
C	14	39.6	4.0	600	12	US-11-136-527-7342	Sequence 7342, Ap
C	15	39.6	4.0	1428	8	US-11-136-527-73246	Sequence 3246, Ap
C	16	38.6	4.0	3924	8	US-10-750-185-24577	Sequence 24577, A
	17	39.6	4.0	3924	8	US-10-750-623-24577	Sequence 24577, A
	18	39.4	4.0	1162	7	US-10-714-887-103	Sequence 103, App
C	19	39.4	4.0	114801	12	US-11-121-086-22	Sequence 22, Appl
	20	39.4	3.9	150468	12	US-11-112-908-56	Sequence 56, Appl
	20	39.2	3.9	150468	12	US-11-112-908-56	Sequence 56, Appl

APPLICANT: POULSEN, TIM S.

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

;; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES

;; FILE REFERENCE: 09138.6000-00000

;; CURRENT APPLICATION NUMBER: US/11/121.086

;; CURRENT FILING DATE: 2005-05-04

;; PRIOR APPLICATION NUMBER: 60/567,570

;; PRIOR FILING DATE: 2004-05-04

;; NUMBER OF SEQ ID NOS: 107

;; SOFTWARE: Patentin version 3.3

;; SEQ ID NO 62

;; LENGTH: 200628

;; TYPE: DNA

;; ORGANISM: Homo sapiens

US-11-121-086-62

Query Match 4.4%; Score 43.6; DB 12; Length 200628;

Best Local Similarity 67.8%; Pred. No. 0.9;

Matches 61; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

QY 166 CCATTCACCATCATCATCACCATCATCAGGACGAGTGTGTGATGACCATGTTCTTC 225

Db 129584 CACCATCATCATCATCACCATCATCAGGACGAGTGTGTGATGACCATGTTCTTC 129643

QY 226 GCCATGGCAACACACACACACACCAT 255

Db 129644 CACCATCATCATCACCACACACCATCAT 129673

#### RESULT 3

US-11-128-061-549

;; Sequence 549, Application US/11/128061

;; Publication No. US20060003958A1

;; GENERAL INFORMATION:

;; APPLICANT: Melville, Mark W.

;; APPLICANT: Charles, Timothy S.

;; APPLICANT: Mounts, William M.

;; APPLICANT: Hann, Louane E.

;; APPLICANT: Sinacore, Martin S.

;; APPLICANT: Leonard, Mark W.

;; APPLICANT: Brown, Eugene L.

;; APPLICANT: Miller, Christopher P.

;; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES RELATED TO OLIGONUCLEOTIDE ARRAYS

;; FILE REFERENCE: 01997.027701

;; CURRENT APPLICATION NUMBER: US/11/128,061

;; CURRENT FILING DATE: 2005-05-11

;; PRIOR APPLICATION NUMBER: US 60/570,425

;; PRIOR FILING DATE: 2004-05-11

;; NUMBER OF SEQ ID NOS: 7285

;; SOFTWARE: Patentin version 3.3

;; SEQ ID NO 549

;; LENGTH: 908

;; TYPE: DNA

;; ORGANISM: Cricetulus sp.

;; FEATURE:

;; NAME/KEY: misc\_feature

;; LOCATION: (29)..(45)

;; OTHER INFORMATION: n is a, c, g, or t

US-11-128-061-549

Query Match 4.2%; Score 41.4; DB 12; Length 908;

Best Local Similarity 57.3%; Pred. No. 0.32;

Matches 75; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

QY 174 CCATCATCATCATCATCAGGACGAGTGTGTGATGACCATGTTCTTCCCATGG 233

Db 58 CCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCA 117

QY 234 CAACACACACACACACCATGGCTGGCAGCAGACTACCCAGTCCACCCGCCGCGCA 293

Db 118 CCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCA 177

QY 294 CAACCTTGACC 304

Db 178 CAAACCCCATC 188

Db 178 CAAACCCCATC 188

#### RESULT 4

US-11-128-049-549

;; Sequence 549, Application US/11/128049

;; Publication No. US20060010513A1

;; GENERAL INFORMATION:

;; APPLICANT: Melville, Mark W.

;; APPLICANT: Mounts, William M.

;; APPLICANT: Hann, Louane E.

;; APPLICANT: Sinacore, Martin S.

;; APPLICANT: Leonard, Mark W.

;; APPLICANT: Brown, Eugene L.

;; APPLICANT: Miller, Christopher P.

;; TITLE OF INVENTION: OLIGONUCLEOTIDE ARRAYS TO MONITOR GENE EXPRESSION AND METHODS FOR

;; FILE REFERENCE: 01997.027700

;; CURRENT APPLICATION NUMBER: US/11/128,049

;; CURRENT FILING DATE: 2005-05-11

;; PRIOR APPLICATION NUMBER: US 60/570,425

;; PRIOR FILING DATE: 2004-05-11

;; NUMBER OF SEQ ID NOS: 7285

;; SOFTWARE: Patentin version 3.3

;; SEQ ID NO 549

;; LENGTH: 908

;; TYPE: DNA

;; ORGANISM: Cricetulus sp.

;; FEATURE:

;; NAME/KEY: misc\_feature

;; LOCATION: (29)..(45)

;; OTHER INFORMATION: n is a, c, g, or t

US-11-128-049-549

Query Match 4.2%; Score 41.4; DB 12; Length 908;

Best Local Similarity 57.3%; Pred. No. 0.32;

Matches 75; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

QY 174 CCATCATCATCATCATCAGGACGAGTGTGTGATGACCATGTTCTTCCCATGG 233

Db 58 CCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCA 117

QY 234 CAACACACACACACACCATGGCTGGCAGCAGACTACCCAGTCCACCCGCCGCGCA 293

Db 118 CCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCA 177

QY 294 CAACCTTGACC 304

Db 178 CAAACCCCATC 188

#### RESULT 5

US-10-995-561-13411

;; Sequence 13411, Application US/10995561

;; Publication No. US20050272054A1

;; GENERAL INFORMATION:

;; APPLICANT: CARGILL, Michele et al.

;; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

;; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF

;; FILE REFERENCE: CL001559

;; CURRENT APPLICATION NUMBER: US/10/995,561

;; CURRENT FILING DATE: 2004-11-24

;; NUMBER OF SEQ ID NOS: 85702

;; SOFTWARE: FastSeq for Windows Version 4.0

;; SEQ ID NO 13411

;; LENGTH: 17263

;; TYPE: DNA

;; ORGANISM: Homo sapiens

US-10-995-561-13411

Query Match 4.1%; Score 41.2; DB 8; Length 17263;

Best Local Similarity 52.3%; Pred. No. 1.4; DB 8; Length 105550;  
Matches 91; Conservative 0; Mismatches 83; Indels 0; Gaps 0;  
QY 126 TTGTGCGGCGCAACAATGCGCGCTCATGTCTCGCCCATTCACCATCATCA 185  
Db 10017 TTGGTTCTGTCAATTAATCATCAACCACTCTCTCACTGCGCACTATTGCCATCATCA 10076  
QY 186 CCATCATCAGGAGCAGCAGCTGTGTGAGTACCAAGTTCTTCGCCCATGGCAACCAACCA 245  
Db 10077 CTACCACTCCACATCAACCTGCCATCATATCATCAGGATCATCAACCAACCACTA 10136  
QY 246 CCACCACTATGGTGGGAGCAGCACTACCAAGTGCACCGCCGCCAGACAATT 299  
Db 10137 CCATTATCCACCATCAACCACTAGAGTTATTACTACCATCACTACAACCAATT 10190

## RESULT 6

US-10-995-561-13234  
; Sequence 13234, Application US/10995561  
; Publication No. US20050272054A1  
; GENERAL INFORMATION:  
; APPLICANT: CARGILL, Michele et al.  
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH  
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF  
; TITLE OF INVENTION: DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001559  
; CURRENT APPLICATION NUMBER: US/10/995,561  
; CURRENT FILING DATE: 2004-11-24  
; NUMBER OF SEQ ID NOS: 85702  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 13234  
; LENGTH: 93112  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1)..(93112)  
; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-  
US-10-995-561-13234

Query Match 4.1%; Score 41.2; DB 8; Length 93112;  
Best Local Similarity 64.9%; Pred. No. 2.9;  
Matches 61; Conservative 0; Mismatches 33; Indels 0; Gaps 0;  
QY 161 TCTGCGCCATTCACCATCATCACTACCATCATCAGGAGCAGCAGTGTGTGATACCACT 220  
Db 83559 TCACCACTCATCACCATTATCATTCACCATCATCACTACCATCATCACTACCACT 83618  
QY 221 TCTGCGCCATTCGCAACCACTACCACTACCACTACCACTACCACTACCACTACCA 254  
Db 83619 ACACCATCATCACTACCACTACCACTACCACTACCACTACCACTACCACTACCA 83652

## RESULT 7

US-10-995-561-13235/c  
; Sequence 13235, Application US/10995561  
; Publication No. US20050272054A1  
; GENERAL INFORMATION:  
; APPLICANT: CARGILL, Michele et al.  
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH  
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF  
; TITLE OF INVENTION: DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001559  
; CURRENT APPLICATION NUMBER: US/10/995,561  
; CURRENT FILING DATE: 2004-11-24  
; NUMBER OF SEQ ID NOS: 85702  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 13235  
; LENGTH: 105550  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-995-561-13235

Query Match 4.1%; Score 41.2; DB 8; Length 105550;  
Best Local Similarity 52.3%; Pred. No. 3.1; DB 8; Length 105550;  
Matches 91; Conservative 0; Mismatches 83; Indels 0; Gaps 0;  
QY 126 TTGTGCGGCGCAACAATGCGCGCTCATGTCTCGCCCATTCACCATCATCA 185  
Db 1028 TTGGTTCTGTCAATTAATCATCAACCACTCTCTCACTGCGCACTATTGCCATCATCA 969  
QY 186 CCATCATCAGGAGCAGCAGCTGTGTGAGTACCAAGTTCTTCGCCCATGGCAACCAACCA 245  
Db 969 CTACCACTCCACATCAACCTGCCATCATATCATCAGGATCATCAACCAACCACTA 909  
QY 246 CCACCACTATGGTGGGAGCAGCACTACCAAGTGCACCGCCGCCAGACAATT 299  
Db 908 CCATTATCCACCATCAACCACTAGAGTTATTACTACCATCACTACAACCAATT 855

## RESULT 8

US-11-010-239-112  
; Sequence 112, Application US/11010239  
; Publication No. US20060015970A1  
; GENERAL INFORMATION:  
; APPLICANT: Roger PENNELL  
; APPLICANT: Jack OKAMURO  
; APPLICANT: Richard SCHNEEBERGER  
; APPLICANT: Yiwen FANG  
; APPLICANT: Shing KWOK  
; APPLICANT: Diane JOFUKU  
; APPLICANT: Edward A. KIEGLE  
; APPLICANT: Jonathan DONSON  
; APPLICANT: Nestor APUYA  
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES AND POLYPEPTIDES ENCODED THEREBY USEFUL FO  
; TITLE OF INVENTION: MODIFYING PLANT CHARACTERISTICS  
; FILE REFERENCE: 2750-1585PUS2  
; CURRENT APPLICATION NUMBER: US/11/010,239  
; CURRENT FILING DATE: 2004-12-09  
; PRIOR APPLICATION NUMBER: US 60/529,352  
; PRIOR FILING DATE: 2003-12-12  
; NUMBER OF SEQ ID NOS: 133  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 112  
; LENGTH: 1544  
; TYPE: DNA  
; ORGANISM: Arabidopsis thaliana  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1)..(1544)  
; OTHER INFORMATION: 12600234\_construct\_ID\_YP0279  
US-11-010-239-112

Query Match 4.1%; Score 41; DB 12; Length 1544;  
Best Local Similarity 56.2%; Pred. No. 0.53;  
Matches 77; Conservative 0; Mismatches 60; Indels 0; Gaps 0;  
QY 543 GAGAGCAGCGAAGGTGATGAGGTATAGGAGAGAGAGAGAGCGCGCTATGACAAGCA 602  
Db 1146 GCGAGAGCAAGTGTGAGGTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1205  
QY 603 AATCGATACGAGTCCAGAAAAGCTTACGCTGAGCTTCGCGCATGGGTCAACGCGCGCTT 662  
Db 1206 AATTCGATACCAAGTTCGAAAAGCTTACGCTGATCAAGCTCTCGAATGAAGGAGCA 1265  
QY 663 TGTCAAGTACCCGAAG 679  
Db 1266 CGTGAGAGGCCCAATG 1282

## RESULT 9

US-10-750-185-27313  
; Sequence 27313, Application US/10750185  
; Publication No. US20050260603A1  
; GENERAL INFORMATION:  
; APPLICANT: MMI GENOMICS, INC.

APPLICANT: DENISE, Sue K.  
APPLICANT: KERR, Richard  
APPLICANT: ROSENFELD, David  
APPLICANT: HOLM, Tom  
APPLICANT: BATES, Stephen  
APPLICANT: FANTIN, Dennis  
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS  
FILE REFERENCE: MM1100-2  
CURRENT APPLICATION NUMBER: US/10/750,185  
CURRENT FILING DATE: 2003-12-31  
PRIOR APPLICATION NUMBER: US 60/437,482  
PRIOR FILING DATE: 2002-12-31  
NUMBER OF SEQ ID NOS: 64922  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 27313  
LENGTH: 7402  
TYPE: DNA  
ORGANISM: Bovine 19866880890824  
US-10-750-185-27313

Query Match 4.1%; Score 40.8; DB 8; Length 7402;  
Best Local Similarity 67.9%; Pred. No. 1.2;  
Matches 57; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

QY 172 CACATCATCATCACCACCATCAGGAGCAGCTGTGAGTACCAAGTTCTTCGGCCAT 231  
Db 1968 CACATCATCATCACCACCATCAGGAGCAGCTGTGAGTACCAAGTTCTTCGGCCAT 231

QY 232 GGCAACCAACCACCAACCACCAT 255  
Db 2028 CATGACCACCATCACCACCATCAT 2051

RESULT 10  
US-10-750-623-27313  
Sequence 27313, Application US/10750623  
Publication No. US20050287531A1  
GENERAL INFORMATION:  
APPLICANT: MMI GENOMICS, INC.  
APPLICANT: DENISE, Sue K.  
APPLICANT: KERR, Richard  
APPLICANT: ROSENFELD, David  
APPLICANT: HOLM, Tom  
APPLICANT: BATES, Stephen  
APPLICANT: FANTIN, Dennis  
TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS  
FILE REFERENCE: MM1100-1  
CURRENT APPLICATION NUMBER: US/10/750,623  
CURRENT FILING DATE: 2003-12-31  
PRIOR APPLICATION NUMBER: US 60/437,482  
PRIOR FILING DATE: 2002-12-31  
NUMBER OF SEQ ID NOS: 64922  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 27313  
LENGTH: 7402  
TYPE: DNA  
ORGANISM: Bovine 19866880890824  
US-10-750-623-27313

Query Match 4.1%; Score 40.8; DB 8; Length 7402;  
Best Local Similarity 67.9%; Pred. No. 1.2;  
Matches 57; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

QY 172 CACATCATCATCACCACCATCAGGAGCAGCTGTGAGTACCAAGTTCTTCGGCCAT 231  
Db 1968 CACATCATCATCACCACCATCAGGAGCAGCTGTGAGTACCAAGTTCTTCGGCCAT 231

QY 232 GGCAACCAACCACCAACCACCAT 255  
Db 2028 CATGACCACCATCACCACCATCAT 2051

RESULT 11

US-09-925-065A-809991  
Sequence 809991, Application US/09925065A  
Publication No. US20040181048A1  
GENERAL INFORMATION:  
APPLICANT: Wang, David G.  
TITLE OF INVENTION: Identification and Mapping of Single  
Nucleotide Polymorphisms in the Human Genome  
FILE REFERENCE: 108827.135  
CURRENT APPLICATION NUMBER: US/09/925,065A  
CURRENT FILING DATE: 2001-08-08  
PRIOR APPLICATION NUMBER: US 60/243,096  
PRIOR FILING DATE: 2000-10-24  
PRIOR APPLICATION NUMBER: US 60/252,147  
PRIOR FILING DATE: 2000-11-20  
PRIOR APPLICATION NUMBER: US 60/250,092  
PRIOR FILING DATE: 2000-11-30  
PRIOR APPLICATION NUMBER: US 60/261,766  
PRIOR FILING DATE: 2001-01-16  
PRIOR APPLICATION NUMBER: US 60/289,846  
PRIOR FILING DATE: 2001-05-09  
NUMBER OF SEQ ID NOS: 957086  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 809991  
LENGTH: 565  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-925-065A-809991

Query Match 4.0%; Score 40; DB 6; Length 565;  
Best Local Similarity 51.9%; Pred. No. 0.63;  
Matches 111; Conservative 1; Mismatches 101; Indels 1; Gaps 1;

QY 138 CAACAACTGCGCGGCTCATGCTCTCGCCCATTCACCATCATCATCATCATCAGGA 197  
Db 12 CCATCACAACCAACCGTCACTACAACTGCGCCCTCCACCATCAGATAACCAAGTCTCCA 71

QY 198 GCACGAGCTGTGTAGTACCA-GTTCTTGGCCCATGGCAACCAACCAACCAACCATG 256  
Db 72 CCAGCACCAGCAGCGGCGCACCACCATCTACAGCCGACCCCTTCACCTTCACCAACCAACCC 131

QY 257 GCTCGCAGCAGACTACCCAGTGCCACCGCCGCGCAGCAACTTCGACCCGCGAGACAT 316  
Db 132 AGTAGTACCGTCACTACAAACCAACCAACCAACCAACCAACCAACCAACCAACCAATTCATCACCAGTCCCAT 191

QY 317 GGACCAAGACCATTTTCATGAACACAGCAGCGCGAGG 350  
Db 192 GGTTAGCCTTCTCTTCTTAACACAAGCAGGAAG 225

RESULT 12  
US-09-925-065A-26496/c  
Sequence 26496, Application US/09925065A  
Publication No. US20040181048A1  
GENERAL INFORMATION:  
APPLICANT: Wang, David G.  
TITLE OF INVENTION: Identification and Mapping of Single  
Nucleotide Polymorphisms in the Human Genome  
FILE REFERENCE: 108827.135  
CURRENT APPLICATION NUMBER: US/09/925,065A  
CURRENT FILING DATE: 2001-08-08  
PRIOR APPLICATION NUMBER: US 60/243,096  
PRIOR FILING DATE: 2000-10-24  
PRIOR APPLICATION NUMBER: US 60/252,147  
PRIOR FILING DATE: 2000-11-20  
PRIOR APPLICATION NUMBER: US 60/250,092  
PRIOR FILING DATE: 2000-11-30  
PRIOR APPLICATION NUMBER: US 60/261,766  
PRIOR FILING DATE: 2001-01-16  
PRIOR APPLICATION NUMBER: US 60/289,846  
PRIOR FILING DATE: 2001-05-09  
NUMBER OF SEQ ID NOS: 957086  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 26496

Query Match 4.0%; Score 40; DB 6; Length 565;  
Best Local Similarity 51.9%; Pred. No. 0.63;  
Matches 111; Conservative 1; Mismatches 101; Indels 1; Gaps 1;

QY 138 CAACAACTGCGCGGCTCATGCTCTCGCCCATTCACCATCATCATCATCATCAGGA 197  
Db 12 CCATCACAACCAACCGTCACTACAACTGCGCCCTCCACCATCAGATAACCAAGTCTCCA 71

QY 198 GCACGAGCTGTGTAGTACCA-GTTCTTGGCCCATGGCAACCAACCAACCAACCATG 256  
Db 72 CCAGCACCAGCAGCGGCGCACCACCATCTACAGCCGACCCCTTCACCTTCACCAACCAACCC 131

QY 257 GCTCGCAGCAGACTACCCAGTGCCACCGCCGCGCAGCAACTTCGACCCGCGAGACAT 316  
Db 132 AGTAGTACCGTCACTACAAACCAACCAACCAACCAACCAACCAACCAACCAACCAATTCATCACCAGTCCCAT 191

QY 317 GGACCAAGACCATTTTCATGAACACAGCAGCGCGAGG 350  
Db 192 GGTTAGCCTTCTCTTCTTAACACAAGCAGGAAG 225

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; LENGTH: 659
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-26496

Query Match
  4.0%; Score 40; DB 6; Length 659;
Best Local Similarity 62.2%; Pred. No. 0.68;
Matches 61; Conservative 1; Mismatches 36; Indels 0; Gaps 0;

QY 157 ATGGTCTGCCCATTCACCATCATCATCACCACCATCAGGAGCAGGAGTGTGTGAGTAC 216
Db 130 ATCTTCTCTTGAACCAACCATCATTCATCACCAYCACCACCAACCAACCAACCAAC 71
QY 217 CAGTTCTTCGCCCATGGCAACCAACCAACCAACCAACCAACCAACCAACCAACCA 254
Db 70 CACCACCACTACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCA 33

RESULT 13
US-09-925-065A-640012/c
; Sequence 640012, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 640012
; LENGTH: 628
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-640012

Query Match
  4.0%; Score 39.8; DB 6; Length 628;
Best Local Similarity 67.5%; Pred. No. 0.76;
Matches 56; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

QY 172 CACCATCATCATCACCACCATCAGGAGCAGGAGTGTGTGAGTACCACTTCTTCCGCCAT 231
Db 270 CACCACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCA 211
QY 232 GGCACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCA 254
Db 210 CACCACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCA 188

RESULT 14
US-11-136-527-7342/c
; Sequence 7342, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26

; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3246
; LENGTH: 1428
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-3246/c
; Sequence 3246, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3246
; LENGTH: 1428
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-3246

Query Match
  4.0%; Score 39.6; DB 12; Length 1428;
Best Local Similarity 63.8%; Pred. No. 1.2;
Matches 60; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

QY 162 CTCGCCCATTCACCATCATCATCACCACCATCAGGAGCAGGAGTGTGTGAGTACCACTT 221
Db 1320 CACACACATACATCATCATCATCAGCATCATCAGCATCATCAGCATCATCAGCATCATCA 1261
QY 222 CTCGCCCATGGCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAAT 255
Db 1260 CCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 1227

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Job time : 406 secs
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GenCore version 5.1.7  
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Run on: February 23, 2006, 11:04:50 ; Search time 810 Seconds

(without alignments)  
1909.103 Million cell updates/sec

Title: US-10-723-947-77

Perfect score: 1048

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Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

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Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1  
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-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA\_Main:

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10: /cgn2\_6/ptodata/1/pubpna/US11\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1035	98.8	996	US-10-723-947-75	Sequence 75, Appl
2	907.5	86.6	975	US-10-723-947-79	Sequence 79, Appl
3	816	77.9	7051	US-10-723-947-74	Sequence 74, Appl
4	768.5	73.3	639	US-10-723-947-88	Sequence 88, Appl
5	756	72.1	642	US-10-723-947-91	Sequence 91, Appl
6	730.5	69.7	639	US-10-723-947-82	Sequence 82, Appl
7	729.5	69.6	639	US-10-723-947-85	Sequence 85, Appl

8	670.5	64.0	2913	8	US-10-723-947-78	Sequence 78, Appl
9	590	56.3	1985	8	US-10-723-947-87	Sequence 87, Appl
10	572.5	54.6	2043	8	US-10-723-947-90	Sequence 90, Appl
11	547.5	52.2	5734	8	US-10-723-947-81	Sequence 81, Appl
12	538	51.3	3454	8	US-10-723-947-84	Sequence 84, Appl
13	258	24.6	864	7	US-10-437-963-83163	Sequence 83163, A
14	237	22.6	901	8	US-10-425-115-34955	Sequence 34955, A
15	232.5	22.2	1413	7	US-10-437-963-82314	Sequence 82314, A
16	207	19.8	1297	3	US-09-770-445-17	Sequence 17, Appl
17	207	19.8	1370	7	US-10-425-114-14597	Sequence 14597, A
18	207	19.8	1404	7	US-10-425-114-13058	Sequence 13058, A
19	204	19.5	972	7	US-10-767-701-11858	Sequence 11858, A
20	194	18.5	1320	7	US-10-437-963-25736	Sequence 25736, A
21	192	18.3	1768	7	US-10-437-963-40	Sequence 40, Appl
22	189.5	18.1	1385	7	US-10-425-114-26389	Sequence 26389, A
23	189.5	18.1	1633	8	US-10-425-115-157740	Sequence 157740, A
24	188	17.9	1101	5	US-10-143-849-7	Sequence 7, Appl
25	186.5	17.8	872	7	US-10-767-701-13864	Sequence 13864, A
26	185.5	17.7	577	7	US-10-260-238-390	Sequence 390, App
27	184.5	17.6	742	8	US-10-425-115-157736	Sequence 157736, A
28	184.5	17.6	1441	8	US-10-739-930-5473	Sequence 5473, Ap
29	181.5	17.3	1396	7	US-10-767-701-12421	Sequence 12421, A
30	180.5	17.2	1101	5	US-10-143-849-5	Sequence 5, Appl
31	180	17.2	698	7	US-10-425-114-14609	Sequence 14609, A
32	180	17.2	1202	7	US-10-425-114-20132	Sequence 20132, A
33	180	17.2	1553	7	US-10-425-114-8013	Sequence 8013, Ap
34	180	17.2	1593	8	US-10-739-930-325	Sequence 225, App
35	179.5	17.1	1139	7	US-10-437-963-101201	Sequence 101201, A
36	177.5	16.9	1415	7	US-10-424-599-33981	Sequence 33981, A
37	176.5	16.8	596	7	US-10-021-323-14874	Sequence 14874, A
38	176.5	16.8	885	3	US-09-938-842A-265	Sequence 265, App
39	176.5	16.8	885	3	US-09-938-842A-265	Sequence 265, App
40	176.5	16.8	1002	7	US-10-280-238-403	Sequence 403, App
41	176.5	16.8	1075	7	US-10-425-114-22406	Sequence 22406, A
42	176.5	16.8	1120	7	US-10-412-699B-597	Sequence 597, App
43	176.5	16.8	1141	5	US-10-295-403-107	Sequence 107, App
44	176.5	16.8	2717	7	US-10-437-963-30197	Sequence 30197, A
45	175	16.7	1124	5	US-10-143-849-1	Sequence 1, Appl

#### ALIGNMENTS

##### RESULT 1

; Sequence 75, Application US/10723947  
; Publication No. US20040205848A1  
; GENERAL INFORMATION:  
; APPLICANT: Dubcovsky, Jorge  
; APPLICANT: Yan, Liuling  
; APPLICANT: Loukianov, Artem  
; TITLE OF INVENTION: GENES RESPONSIBLE FOR VERNALIZATION AND USES THEREOF  
; FILE REFERENCE: 514112000320  
; CURRENT APPLICATION NUMBER: US/10/723,947  
; CURRENT FILING DATE: 2003-11-26  
; PRIOR FILING DATE: 2003-04-11  
; NUMBER OF SEQ ID NOS: 159  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 75  
; LENGTH: 996  
; TYPE: DNA  
; ORGANISM: Triticum monococcum  
US-10-723-947-75

##### Alignment Scores:

Pred. No.: 1.56e-111 Length: 996  
Score: 1035.00 Matches: 185  
Percent Similarity: 99.5% Conservative: 1  
Best Local Similarity: 98.9% Mismatches: 1  
Query Match: 98.8% Indels: 0  
DB: 8 Gaps: 0



2

US-10-723-947-77 (1-187) x US-10-723-947-74 (1-7051)

Qy	1	MetSerMetSerCysGlyLeuCysGlyAlaAsnAsnCysProArgLeuMetValSerPro	20
Db	3001	ATGTCCATGTGTCGGGCTTTGTGGCGGCCCAACAACATGCCGGCGCTCATGGTCTCGCCC	3060
Qy	21	IleHisHisHisHisHisHisHisGlnLeuHisGlnLeuCysGluTyrGlnPhePheAla	40
Db	3061	ATTCAACATCATCATCAACATCATCAGGAGCACCAGCTGTGTGAGTACCAAGTCTCTTCGCC	3120
Qy	41	HisGlyAsnHisHisHisHisHisHisGlySerAlaAlaAspTyrProValProProPro	60
Db	3121	CATGGCAACACCACCAACCAACCATATGGTTCGGCAGCAGACTACCCAGTGCACCGCCG	3180
Qy	61	ProAspAsnPheAspHisAsArgThrTyrThrArgProPheHisGluThrAlaAlaAla	80
Db	3181	CCAGACAACTTCGACCAACCCAGACACATGACCGACCACTTTTATGAAACAGCAGCGGCA	3240
Qy	81	GlyAsnSerSerArgLeuThrLeuGluValGlyAlaGlyGlyGlnHisMetAlaHisLeu	100
Db	3241	GGGAACAGCAGCAGGCTCACGCTGGAGTGGCGCAGCGCCCAACACATGGCTCACCTA	3300
Qy	101	ValClnProProAlaArgAlaHisIle	109
Db	3301	GTGCAGCACCGGACAGGCCACATCGTAAGTAGTACTACTGCTTAATTTGTTTCATCTC	3360
Qy	109	-----	109
Db	3361	TTCCGATGGATGGTCCATGGCTTCCTCTTAAATAATCCCACTAAATTAATGTCCATC	3420
Qy	109	-----	109
Db	3421	TGACTACACCCACTACAAAAAGTAGCACCATGTAAACATTTTCATATATTCTCACATAA	3480
Qy	109	-----	109
Db	3481	TTCTGTTAATTTAGCGTCTCGATTGTTCTCTGAAAGAAATATACGGGAATGGATCTGG	3540
Qy	109	-----	109
Db	3541	ATATTTCTTTAATTTCTATGGAGCATAGAGTTTGTTGTTATTAGTTGATGCAGAAAT	3600
Qy	109	-----	109
Db	3601	TGTATGGTTGTCAAATCATCATCATATATATATATTTCTTTTGTGCACTTAATACTA	3660
Qy	109	-----	109
Db	3661	AAGNAGTAATCAGTCATCATCATGCACTGAAAAATTAGACTTGTGTCAATAACTAACTA	3720
Qy	109	-----	109
Db	3721	ACCAACTCGACCGCACAGCTGGGGGAAGACTTTTAATCAAAGCTCTAGCTAGAGCTTAAT	3780
Qy	109	-----	109
Db	3781	AATATAACATATCTCTTTATGGGATCAAGCAATACATATCGGCTCAATTTCTCAACTTGC	3840
Qy	109	-----	109
Db	3841	AATATCTATCTGGAGTCCACACTTTATGGTAAATTAATTGACAAAAGTTTTGTGAAATGGAC	3900
Qy	109	-----	109
Db	3901	AATATACATATCGGATCGATGCACCCCTTTTCTCATTTTATGTGGTCATTATAATTGATT	3960
Qy	109	-----	109
Db	3961	GTTATTTAGTATTTCAATTTTATCTTGAGCTAGTTTTTGCAAGTCTGTAGCTCATATATAA	4020
Qy	109	-----	109
Db	4021	CTGATACTACTCCCCACGATAGTTGGGTAGTGGCGGGGTATCGATCTACTACCGATTTCAT	4080

## RESULT 4

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US-10-723-947-88
; Sequence 88, Application US/10723947
; Publication No. US20040205848A1
; GENERAL INFORMATION:
; APPLICANT: Dubcovsky, Jorge
; APPLICANT: Yan, Liuling
; APPLICANT: Loukoianov, Artem
; TITLE OF INVENTION: GENES RESPONSIBLE FOR VERNALIZATION
; AND USES THEREOF
; TITLE OF INVENTION: REGULATION IN TEMPERATE GRASSES AND
; FILE REFERENCE: 514112000320
; CURRENT APPLICATION NUMBER: US/10/723,947
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US 10/412,137
; PRIOR FILING DATE: 2003-04-11
; NUMBER OF SEQ ID NOS: 159
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 88
; LENGTH: 639
; TYPE: DNA

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ORGANISM: Hordeum vulgare  
US-10-723-947-88

## Alignment Scores:

Pred. No.: 2,086-80 Length: 639  
Score: 768.50 Matches: 148  
Percent Similarity: 82.6% Conservatives: 9  
Best Local Similarity: 77.9% Mismatches: 28  
Query Match: 73.3% Indels: 5  
DB: 8 Gaps: 3

US-10-723-947-77 (1-187) x US-10-723-947-88 (1-639)

```
QY 1 MetSerMetSerCysGlyLeuCysGlyAlaAsnAsnCysProArgLeuMetValSerPro 20
DB 1 ATGTCCATGTGCATGTGTTGTGCGCGCCAGCAACTGCGGTACACATGATGTGCGCC 60
QY 21 IleHisHisHisHisHisHisHisHisHisHisHisHisHisHisHisHisHisHis 40
DB 61 GTTCTTCTTCATCATCACCATCATCAGGAACACCCACTGCACGAGTACCAGTTCTTCGCC 120
QY 41 HisGlyAsnHisHisHisHisHisHisHisHisHisHisHisHisHisHisHisHisHis 59
DB 121 CAAGGT-----CACCAACACACACAGCGCGGCGGAGGACTACCCACACACCGCCCA 174
QY 60 ProProAspAsnPheAspHisArgArgThrTrpThrArgProPheHisGluThrAlaAla 79
DB 175 CGCCAGACAAATGTCACACACACACATCATGACACCGCGCTTTCATGAACAGCAGCT 234
QY 80 AlaGlyAsnSerSerArgLeuThrLeuGluValGlyAlaGlyGlyGlnHisMetAlaHis 99
DB 235 CCAGAGAACAGACACAGCGGTTCACACGGGAGGTGGACGCGCGGCCCAACACATGGCTCAC 294
QY 100 LeuValGlnProProAla-----ArgAlaHisIleValProPheTyrGlyGlyAlaPhe 117
DB 295 CTGCTCGACCCACCGCGCGCCGCGCCAGACCAACCATCTGTCGCATTCGCGAGAGTGATTC 354
QY 118 ThrAsnThrIleSerAsnGluAlaIleMetThrIleAspThrGluMetMetValGlyPro 137
DB 355 GCCAGCACTATTAGCAACGCAACGATCATGACTATTGATACAGAAATGATGGTGGCGCT 414
QY 138 AlaHisTyrProThrMetGlnGluArgAlaAlaLysValMetArgTyrArgGluLysArg 157
DB 415 GCCTATATCCACAGATGCAGGAGAGAGAGGCGGAAGGTGATGAGGTACAGGGAGAGAGG 474
QY 158 LysArgArgArgTyrAspLysGlnIleArgTyrGluSerArgLysAlaTyrAlaGluLeu 177
DB 475 NAGAGCGCGGCTATGACAGCAAAATCCGCTACGAGTCCAGAAAGCTTACGCCGAGCTC 534
QY 178 ArgProArgValAsnGlyArgPheValLys 187
DB 535 AGGCCACGGGTCAATGCGCGCTTTGCAAG 564
```

## RESULT 5

US-10-723-947-91

Sequence 91, Application US/10723947  
Publication No. US20040205848A1

## GENERAL INFORMATION:

APPLICANT: Dubcovsky, Jorge

APPLICANT: Yan, Liuling

APPLICANT: Loukoianov, Artem

TITLE OF INVENTION: GENES RESPONSIBLE FOR VERNALIZATION

TITLE OF INVENTION: REGULATION IN TEMPERATE GRASSES AND USES THEREOF

FILE REFERENCE: 514112000320

CURRENT APPLICATION NUMBER: US/10/723,947

PRIOR FILING DATE: 2003-11-26

PRIOR FILING DATE: 2003-04-11

NUMBER OF SEQ ID NOS: 159

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 91

LENGTH: 642

TYPE: DNA

ORGANISM: Hordeum vulgare  
US-10-723-947-91

## Alignment Scores:

Pred. No.: 6,218-79 Length: 642  
Score: 756.00 Matches: 146  
Percent Similarity: 82.6% Conservatives: 11  
Best Local Similarity: 76.8% Mismatches: 29  
Query Match: 72.1% Indels: 4  
DB: 8 Gaps: 3

US-10-723-947-77 (1-187) x US-10-723-947-91 (1-642)

```
QY 1 MetSerMetSerCysGlyLeuCysGlyAlaAsnAsnCysProArgLeuMetValSerPro 20
DB 1 ATGTCCATGTGCATGTGTTGTGCGCGCCAGCAAAATGCGCGTATCACATGATGTGCGCC 60
QY 21 IleHisHisHisHisHisHisHisHisHisHisHisHisHisHisHisHisHisHis 40
DB 61 GTTCTTCTTCATCATCACCATCATCAGGAACATCGGACGCGGAGTACCAGTTCTTCGCC 120
QY 41 HisGlyAsnHisHisHisHisHisHisHisHisHisHisHisHisHisHisHisHisHis 59
DB 121 CAAGGT-----CACCAACACACACAGCGCGGCGGAGGACTACCCACCGCCACAGCCA 177
QY 60 ProProAspAsnPheAspHisArgArgThrTrpThrArgProPheHisGluThrAlaAla 79
DB 178 CGCGCGCGCAATGTCACACCGCAGATCATGCGGCCACGCTGTTTCATGAACAGCAGCT 237
QY 80 AlaGlyAsnSerSerArgLeuThrLeuGluValGlyAlaGlyGlyGlnHisMetAlaHis 99
DB 238 CCAGTGAATAGCACAGCGGTTCACACAGAGGTGGACGCGCGGCCCAACAGATGGCTCAC 297
QY 100 LeuValGlnProProAla-----ArgAlaHisIleValProPheTyrGlyGlyAlaPhe 117
DB 298 CTGCTGCGACCAACCGCGCGCCGCGCCAGACCAACCATCTGTCGCATTCGCGCGGAGTGATTC 357
QY 118 ThrAsnThrIleSerAsnGluAlaIleMetThrIleAspThrGluMetMetValGlyPro 137
DB 358 ACCAACACTATTAGCAACGCAACGATCATGACTATTGATACAGAGATGATGGCGGGACT 417
QY 138 AlaHisTyrProThrMetGlnGluArgAlaAlaLysValMetArgTyrArgGluLysArg 157
DB 418 GCCTATATCCACAGATGCAGGAGAGAGAGGCGGAAGGTGATGAGGTACAGGGAGAGAGG 477
QY 158 LysArgArgArgTyrAspLysGlnIleArgTyrGluSerArgLysAlaTyrAlaGluLeu 177
DB 478 NAGAGCGCGGCTATGACAGCAAAATCCGCTACGAGTCCAGAAAGCTTACGCCGAGCTT 537
QY 178 ArgProArgValAsnGlyArgPheValLys 187
DB 538 AGGCCACGGGTCAACGCGCGCTTTGCAAG 567
```

## RESULT 6

US-10-723-947-82

Sequence 82, Application US/10723947  
Publication No. US20040205848A1

## GENERAL INFORMATION:

APPLICANT: Dubcovsky, Jorge

APPLICANT: Yan, Liuling

APPLICANT: Loukoianov, Artem

TITLE OF INVENTION: GENES RESPONSIBLE FOR VERNALIZATION

TITLE OF INVENTION: REGULATION IN TEMPERATE GRASSES AND USES THEREOF

FILE REFERENCE: 514112000320

CURRENT APPLICATION NUMBER: US/10/723,947

PRIOR FILING DATE: 2003-11-26

PRIOR FILING DATE: 2003-04-11

NUMBER OF SEQ ID NOS: 159

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 82

LENGTH: 639

TYPE: DNA

ORGANISM: Triticum monococcum  
US-10-723-947-82

Alignment Scores:  
Pred. No.: 6,21e-76 Length: 639  
Score: 730.50 Matches: 144  
Percent Similarity: 81.6% Conservative: 11  
Best Local Similarity: 75.8% Mismatches: 28  
Query Match: 69.7% Indels: 7  
DB: 8 Gaps: 4

US-10-723-947-77 (1-187) x US-10-723-947-82 (1-639)

QY 1 MetSerMetSerCysGlyLeuValAlaAsnAsnCysProArgLeuMetValSerPro 20  
DB 1 ARGTCATGTCATGCGGTTGTGCGGCGCAAGCGACTGCCCGCACCACATGATCTCGCCC 60  
QY 21 IleHisHisHisHisHisHisHisGlnGluHisGlnLeuCysGluTyrGlnPhePheAla 40  
DB 61 GTT-----CTTCAGCATCAGAACACACACTGCGTGGCGAGTACCAGTTCTTCACC 111  
QY 41 HisGlyAsnHisHisHisHisHisHisGlySerAlaAlaAspTyrProValProProPro 60  
DB 112 CAAGGC---CACACACACACACACCGCGCGCGGCGGACTTACCACCGCCCGCCCA 168  
QY 61 ProAsp---AsnPheAspHisArgArgThrTTPThrArgProPheHisGluThrAlaAla 79  
DB 169 CCGTCGGCGCAATGGCCACCTGCAGATCATGGACCAACACCGCTTTCATGAACACAGCAGCT 228  
QY 80 AlaGlyAsnSerSerArgLeuThrLeuGluValGlyAlaGlyGlyGlnHisMetAlaHis 99  
DB 229 GCAGGGAACAGCAGCAGACTCAGCTGGAGGTAGTAGCGGCGGCGGCAACATGGCTCAC 288  
QY 100 LeuValGlnProProAlaAlaAlaHis-----IleValProPheTyrGlyGlyAlaPhe 117  
DB 289 CTGCTGCAGCCACCGCGCACCGCAAGAACACCACTCGTCCCATTCCTGCGGGGCTGCATTC 348  
QY 118 ThrAsnThrIleSerAsnGluAlaIleMetThrIleAspThrGluMetMetValGlyPro 137  
DB 349 ACCAGCATATTAGCAATGCACATCATGATCATGATTTATGATACAGATGATGGTGGGGCT 408  
QY 138 AlaHisTyrProThrMetGlnGluArgAlaAlaLysValMetArgTyrArgGluLysArg 157  
DB 409 GCCCATATCTCAGCATGCAGGAGAGAGAGCGGAGGCGAGGTGATGAGGTACAGGAGAGAGG 468  
QY 158 LysArgArgArgTyrAspLysGlnIleArgTyrGluSerArgLysAlaTyrAlaGluLeu 177  
DB 469 AAGAGCGGTGCTATGACAAGCAAAATCCGCTACGAGTCCAGAAAAGCTTACGCCGAGCTC 528  
QY 178 ArgProArgValAsnGlyArgPheValLys 187  
DB 529 AGGCCACGGGTCAATGGCGCTTTGTCAAG 558

RESULT 7  
US-10-723-947-85  
; Sequence 85, Application US/10723947  
; Publication No. US20040205848A1  
; GENERAL INFORMATION:  
; APPLICANT: Dubcovsky, Jorge  
; APPLICANT: Yan, Liuling  
; APPLICANT: Loukoianov, Artem  
; TITLE OF INVENTION: GENES RESPONSIBLE FOR VERNALIZATION  
; FILE OF INVENTION: REGULATION IN TEMPERATE GRASSES AND USES THEREOF  
; FILE REFERENCE: 514112000320  
; CURRENT APPLICATION NUMBER: US/10/723,947  
; CURRENT FILING DATE: 2003-11-26  
; PRIOR FILING DATE: 2003-04-11  
; NUMBER OF SEQ ID NOS: 159  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 85  
; LENGTH: 639  
; TYPE: DNA

ORGANISM: Triticum dicoccoides  
US-10-723-947-85

Alignment Scores:  
Pred. No.: 8,15e-76 Length: 639  
Score: 729.50 Matches: 143  
Percent Similarity: 81.6% Conservative: 12  
Best Local Similarity: 75.3% Mismatches: 28  
Query Match: 69.6% Indels: 7  
DB: 8 Gaps: 4

US-10-723-947-77 (1-187) x US-10-723-947-85 (1-639)

QY 1 MetSerMetSerCysGlyLeuValAlaAsnAsnCysProArgLeuMetValSerPro 20  
DB 1 ARGCCCATGTCATGCGGTTGTGCGGCGCAAGCGACTGCCCGCACCACATGATCTCGCCC 60  
QY 21 IleHisHisHisHisHisHisHisGlnGluHisGlnLeuCysGluTyrGlnPhePheAla 40  
DB 61 GTT-----CTTCAGCATCAGAACACACACTGCGTGGCGAGTACCAGTTCTTCACC 111  
QY 41 HisGlyAsnHisHisHisHisHisHisGlySerAlaAlaAspTyrProValProProPro 60  
DB 112 CAAGGC---CACACACACACACACCGCGCGGCGGCGGACTTACCACCGCCCGCCCA 168  
QY 61 ProAsp---AsnPheAspHisArgArgThrTTPThrArgProPheHisGluThrAlaAla 79  
DB 169 CCGTCAGCAATGGCCACCTGCAGATCATGGACCAACACCGCTTTCATGAACACAGCAGCT 228  
QY 80 AlaGlyAsnSerSerArgLeuThrLeuGluValGlyAlaGlyGlyGlnHisMetAlaHis 99  
DB 229 GCAGGGAACAGCAGCAGGCTCAGCTGGAGGTAGTAGCGGCGGCGGCAACATGGCTCAC 288  
QY 100 LeuValGlnProProAlaAlaAlaHis-----IleValProPheTyrGlyGlyAlaPhe 117  
DB 289 CTGCTGCAGCCACCGCGCACCGCAAGAACACCACTCGTCCCATTCCTGCGGGGCTGCATTC 348  
QY 118 ThrAsnThrIleSerAsnGluAlaIleMetThrIleAspThrGluMetMetValGlyPro 137  
DB 349 ACCAGCATATTAGCAATGCACATCATGATCATGATTTATGATACAGATGATGGTGGGGCT 408  
QY 138 AlaHisTyrProThrMetGlnGluArgAlaAlaLysValMetArgTyrArgGluLysArg 157  
DB 409 GCCCATATCTCAGCATGCAGGAGAGAGAGCGGAGGCGAGGTGATGAGGTACAGGAGAGAGG 468  
QY 158 LysArgArgArgTyrAspLysGlnIleArgTyrGluSerArgLysAlaTyrAlaGluLeu 177  
DB 469 AAGAGCGGTGCTATGACAAGCAAAATCCGCTATGATGATCCAGAAAAGCTTACGCCGAGCTC 528  
QY 178 ArgProArgValAsnGlyArgPheValLys 187  
DB 529 AGGCCACGGGTCAATGGCGCTTTGTCAAG 558

RESULT 8  
US-10-723-947-78  
; Sequence 78, Application US/10723947  
; Publication No. US20040205848A1  
; GENERAL INFORMATION:  
; APPLICANT: Dubcovsky, Jorge  
; APPLICANT: Yan, Liuling  
; APPLICANT: Loukoianov, Artem  
; TITLE OF INVENTION: GENES RESPONSIBLE FOR VERNALIZATION  
; FILE OF INVENTION: REGULATION IN TEMPERATE GRASSES AND USES THEREOF  
; FILE REFERENCE: 514112000320  
; CURRENT APPLICATION NUMBER: US/10/723,947  
; CURRENT FILING DATE: 2003-11-26  
; PRIOR FILING DATE: 2003-04-11  
; NUMBER OF SEQ ID NOS: 159  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 78  
; LENGTH: 2913  
; TYPE: DNA

ORGANISM: Triticum dicoccoides  
US-10-723-947-78

## Alignment Scores:

Pred. No.: 5,32e-68 Length: 2913  
Score: 670.50 Matches: 168  
Percent Similarity: 28.3% Conservative: 3  
Best Local Similarity: 27.8% Mismatches: 9  
Query Match: 64.0% Indels: 424  
DB: 8 Gaps: 2

US-10-723-947-77 (1-187) x US-10-723-947-78 (1-2913)

```
QY 1 MetSerMetSerCysGlyLeuCysGlyAlaAsnAsnCysProArgLeuMetValSerPro 20
DB 578 ATGTCCATGTGTCGGTGTGTGCGGGCCCAACAACTGCCCGCGCTCATGTCTCGCCC 637
QY 21 IleHisHisHisHisHisHisHisHisHisHisHisHisHisHisHisHisHisHis 40
DB 638 ATTTCATCATGTCATCACCATCATCAGGAGCAGCAGCTGCTCAGCAGCAGCTTCTTCGCC 697
QY 41 HisGlyAsnHisHisHisHisHisHisHisHisHisHisHisHisHisHisHisHisHis 60
DB 698 CAAAGGCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAAC 736
QY 61 ProAspAsnPheAspHisArgArgThrTrpThrArgProPheHisGluThrAlaAlaAla 80
DB 737 CCAGCCAACTTCGACCATAGCAGAAACATGGACCAACCACTTCATGAACAGCAGCTGCA 796
QY 81 GlyAsnSerSerArgLeuThrLeuGluValGlyAlaGlyGlyGlnHisMetAlaHisLeu 100
DB 797 GGGAAACAGCAGCAGGCTCAGCTGGAGGTGGGGCGGCGGCGGCGGCGGCGGCGGCGGCT 856
QY 101 ValGlnProProAlaAlaAlaAlaHisHisHisHisHisHisHisHisHisHisHisHis 109
DB 857 GTGACGCCACCGGCAAGAGCCCAACATCGTAAGTAGTAGTACCGCTTAATGTTTTCATCTC 916
QY 109 ----- 109
DB 917 TTGCCGATGGATCGTCCCTCGGCTCTCTCTTAAATAATCCCACTTAATTATGTCATC 976
QY 109 ----- 109
DB 977 TATACCCACTACAAAAAATAGCACCATGTAAACCATCTCATATATCTGTGCAGATAATCT 1036
QY 109 ----- 109
DB 1037 GTTAATGTACGGTCTCAATTTGTTCTCTGAAAAAGATATGCGGGGAATGGATCTTGATAT 1096
QY 109 ----- 109
DB 1097 TCTTTAATTTCTATGGAGCATATATAGAGTTTGTGTTTGTATTAGTTGATGAGAT 1156
QY 109 ----- 109
DB 1157 TGTATGGGTTGTCAAAATCATCATGATCATATATAAACTTATTTCATTTTATTGACCAAC 1216
QY 109 ----- 109
DB 1217 AACAGGTAATCAGTCATCATGCTACTGTAATTTGACTTGTGTTCAATTAACCAACCA 1276
QY 109 ----- 109
DB 1277 ACTCGAGCGGACAGCTGGGGAGAGACTTTAATCAAGCTGTAGCTAGAGCTTAATAATA 1336
QY 109 ----- 109
DB 1337 TAACATATCTTTATGGGATCAAGCAATACATATGCGCTCAATTTCTCAACTTGTCAATA 1396
QY 109 ----- 109
DB 1397 TCTATCTGGAGTCCACACTTTATGGTAATTAATGTGACAAAGTTTTGTGAAATGGACAATA 1456
```

```
QY 109 ----- 109
DB 1457 TACATACTGGATCGATGCACCCCTTTTCTCATTTTATGTGGTCATTTATGAATTTGATTGT 1516
QY 109 ----- 109
DB 1517 TATTTAGTATTTCAATTTTATCTTGAGCTAGTGTTCGCAAGTCTGTAGCTCATATATAACT 1576
QY 109 ----- 109
DB 1577 GATACTACTCCCAACGATAGCTTTCGTAGTGGCGGGTGCATCTACCGAGTTCATATAA 1636
QY 109 ----- 109
DB 1637 AACTGATCGAGATCGGTCCAAAAAAGAAACAAACCCATACAAAAATGGAAGAAAGATCCTT 1696
QY 109 ----- 109
DB 1697 GTTTAGTGTAGTTGCATCAGAAAAATGGCTAATTAGTTACTTTGCTATCAATCTTTTGAAC 1756
QY 109 ----- 109
DB 1757 ATGGCATGTTACCCCCAACGCACTCAGATCACAATTTATTGATGAAGTTACGCTTTTAA 1816
QY 109 ----- 109
DB 1817 AACTCATAAAACTGTACATACATGTACAGGCTACACACATGTACATAATACACCTAAT 1876
QY 109 ----- 109
DB 1877 TAAAAAGTATATTCGTAGACCAATTTGTTGGACGGTGCACATCTTTGAAAAAATATGCC 1936
QY 109 ----- 109
DB 1937 AGAGGAGTTGTAGCTTCCACTGTCCAGAAATAGTAATAGTTACAATCAAGTGCATCTCTG 1996
QY 109 ----- 109
DB 1997 AATGAAATGGATCATTTTCTAGTTAATTAGAGACCAATTAGATACTTCAATAACAGGGG 2056
QY 109 ----- 109
DB 2057 AGTATCAAGTAGTATCTGTCTACCTTAAGAAAGTACATACTGCGATCTTATGATTATTT 2116
QY 110 -----ValProPheThrGlyAlaPheThrAsnThrIleSerAsnG 124
DB 2117 TCCTCTTCATGTTTCAGTGGCCATTTTACGAGGTGCATTCACCAACATATTAGCAATGA 2176
QY 124 uAlaIleMetThrIleAspThrGluMetMetValGlyProAlaHisIleThrProThrMetG 144
DB 2177 AGCAATCATGACTATTGACACAGAGATGATGTTGGGGCTGCCCATTTATCCCAATGCA 2236
QY 144 nGluArgAlaAlaLysValMetArgTyrArgGluLysArgLysArgGlyTyrAspLys 164
DB 2237 GGAGAGACAGCAAGGTGATGAGGTATAGGGAAGAGAGAGGCGCGCTATGACAA 2296
QY 164 sGlnIleArgTyrGluSerArgLysAlaTyrAlaGluLeuArgProArgValAsnGlyArg 184
DB 2297 GCNAATCAGATACAGTCCAGAAAGCTTACGCTGAGCTTCGCGCCACCGGCTCAACGGCTG 2356
QY 184 gPheValLys 187
DB 2357 CTTTGTCAAG 2366
```

## RESULT 9

US-10-723-947-87  
; Sequence 87, Application US/10723947  
; Publication No. US20040205848A1  
; GENERAL INFORMATION:  
; APPLICANT: Dubcovsky, Jorge  
; APPLICANT: Yan, Liuling  
; APPLICANT: Loukoianov, Artem  
; TITLE OF INVENTION: GENES RESPONSIBLE FOR VERNALIZATION

1 TITLE OF INVENTION: REGULATION IN TEMPERATE GRASSES AND USES THEREOF

2 FILE REFERENCE: 514112000320  
3 CURRENT APPLICATION NUMBER: US/10/723,947  
4 CURRENT FILING DATE: 2003-11-26  
5 PRIOR APPLICATION NUMBER: US 10/412,137  
6 PRIOR FILING DATE: 2003-04-11  
7 NUMBER OF SEQ ID NOS: 159  
8 SOFTWARE: FastSeq for Windows Version 4.0  
9 SEQ ID NO 87  
10 LENGTH: 1985  
11 TYPE: DNA  
12 ORGANISM: Hordeum vulgare  
13 US-10-723-947-87

Alignment Scores:  
Pred. No.: 9.68e-59 Length: 1985  
Score: 590.00 Matches: 147  
Percent Similarity: 29.6% Conservative: 9  
Best Local Similarity: 27.9% Mismatches: 29  
Query Match: 56.3% Indels: 342  
DB: 8 Gaps: 4

US-10-723-947-77 (1-187) x US-10-723-947-87 (1-1985)

QY 1 MetSerMetSerCysGlyLeuCysGlyAlaAsnAsnCysProArgLeuMetValSerPro 20  
DB 336 ATGTCATGTCATGTTGTTGGCGCGCCGCACTGCGTACCAATGATGTCGCC 395  
QY 21 IleHisHisHisHisHisHisGlnGluHisGlnLeuCysGlyPyrGlnPheAla 40  
DB 396 GTTCTCTTTCATCATCACCATCATCAGGAACACCCACTGCACGAGTACCACTCTTCGCC 455  
QY 41 HisGlyAsnHisHisHisHisHisHisGlySerAlaAlaAspTyr---ProValProPro 59  
DB 456 CAAGGT-----CACCAACACCAACACGCGCGGCGGAGCTTACCCACCAACCGCCA 509  
QY 60 ProProAspAsnPheAspHisArgArgThrTrpThrArgProPheHisGluThrAlaAla 79  
DB 510 CGCCGAGCAATGCGCACCAACACAGATCATGGACCCAGCGCTTTCATGAAACAGCAGCT 569  
QY 80 AlaGlyAsnSerArgLeuThrLeuGluValGlyAlaGlyGlyGlnHisMetAlaHis 99  
DB 570 CCAGAGAACAGACACAGGCTCACACGGAGGTGGACGCGGCGGCAACACATGGCTCAC 629  
QY 100 LeuValGlnProProAla----- 105  
DB 630 CTGCTGCAGCCACCGCGCGCCGCAAGAGCCACCATCGTGAGTAGTACTACTGCTTAATTT 689  
QY 105 ----- 105  
DB 690 TTCTATCTCTGCGGATCGATGGGACCTGCTAACAAAATCACACTTCTTAATTTCCAT 749  
QY 105 ----- 105  
DB 750 CTCAAAAAAGCTACCGCATGTGACCGCTCATATATATATGCCATAACTCCTTTAATTT 809  
QY 105 ----- 105  
DB 810 TATTCTGTCGATGTGAATTTACCAAGGAGAAAGCTTGATTTTGTATCAGTTGATGCA 869  
QY 105 ----- 105  
DB 870 CAAGAATGGCGCTACGTCATCAGTCGCACATATATATATTTATTTTATTTTGA 929  
QY 105 ----- 105  
DB 930 CTAACAAGTAAGTAAATTCCTTTATGGGTCAAGCAATACATATGTGCACGCGCTTC 989  
QY 105 ----- 105  
DB 990 ATGTTAATTCCTTGACAAAGTTTGTGAAGTGGAAAAATATATTTTATTTATCAATGCACCT 1049  
QY 105 ----- 105

## RESULT 10

US-10-723-947-90  
; Sequence 90, Application US/10723947  
; Publication NO. US20040205848A1  
; GENERAL INFORMATION:  
; APPLICANT: Dubcovsky, Jorge  
; APPLICANT: Yan, Liuling  
; APPLICANT: Loukoianov, Artem  
; TITLE OF INVENTION: GENES RESPONSIBLE FOR VERNALIZATION  
; TITLE OF INVENTION: REGULATION IN TEMPERATE GRASSES AND USES THEREOF  
; FILE REFERENCE: 514112000320  
; CURRENT APPLICATION NUMBER: US/10/723,947  
; CURRENT FILING DATE: 2003-11-26  
; PRIOR APPLICATION NUMBER: US 10/412,137

DB 1050 ACTCTCAITTTATGTTGGTCAITTTATGAATTTTATTAATTTTCTGTTGAGCTAGTTTGTGA 1109  
QY 105 ----- 105  
DB 1110 TCGTTATAGCTCATATATAACTGATACTACTCCCATATAATTTTCCGTAGTGGTCGGGTG 1169  
QY 105 ----- 105  
DB 1170 ATCGATCTACCTAGTTTCATAAACTTATCGAGATCAGGTCCAAAAACAGACCAAAACCTCAC 1229  
QY 105 ----- 105  
DB 1230 GAAATGGAACAAGATCCTTGTGTTAATTAATTTAGTTTGCATCAGGAAATGCTTATTACTTGCT 1289  
QY 105 ----- 105  
DB 1290 GTCAATCTTTATGAAGATGTAATTTTCTCACAATGGATCCAGTCAAAATTTGTGTGAA 1349  
QY 106 -----ArgAlaHisIle----- 109  
DB 1350 GTTAAACATTTTGGCAATTCATAAACCGTGCATAGATGTCCGGCTACACGCACACAAG 1409  
QY 109 ----- 109  
DB 1410 TACATAATACACTAGTTAAACATATATATCCATAGAGCAATTTGAGTTTGGACTATGGCT 1469  
QY 109 ----- 109  
DB 1470 TCATTGGACACAAGGCCCGGGAAGTTGTTCTCTTCATTGTCTAAAAAATAGAACAGT 1529  
QY 109 ----- 109  
DB 1530 TACAGTCAAGTCCAACACTGAATGAATGAATGGATCAAGTTTGTGTTAAACAGACCAACT 1589  
QY 109 ----- 109  
DB 1590 TATCTTCTATAAACAGGAATATCAAGTACATATCTGCTACCCACCAAGAAAAGTACACCT 1649  
QY 110 -----ValProPheTyrGlyGlyAlaPheThrAsnThr 120  
DB 1650 TATGACTATTTTCTTCTTGTATGTTCCAGGTGCCATTTCTGCGAGAGTGCATTCGCCAGCACT 1709  
QY 121 IleSerAsnGluAlaIleMetThrIleAspThrGluMetMetValGlyProAlaHisTyr 140  
DB 1710 ATTAGCAACGCAACATCATGACTATTGATACAGAAATGATGGTGGGCTGCTTAAT 1769  
QY 141 ProThrMetGlnGluArgAlaAlaLysValMetArgTyrArgGluLysArgLysArgArg 160  
DB 1770 CCAACGATGCAGGAGAGAGCGGGAAGGTGATGAGGTACAGGAGAGAGAGAGAGCGG 1829  
QY 161 ArgTyrAspLysGlnIleArgTyrGluSerArgLysAlaTyrAlaGluLeuArgProArg 180  
DB 1830 CGCTATGACAAGCAAAATCCGCTACGAGTCCAGAAAAGCTTACGCCGAGCTCAGGCCACGG 1889  
QY 181 ValAsnGlyArgPheValLys 187  
DB 1890 GTCAATGGCGCTTGGCCAAG 1910

FILE REFERENCE: 314112000320  
CURRENT APPLICATION NUMBER: US/10/723,947

```
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US 10/412,137
; PRIOR FILING DATE: 2003-04-11
; NUMBER OF SEQ ID NOS: 159
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 81
; LENGTH: 5734
; TYPE: DNA
; ORGANISM: Triticum monococcum
; US-10-723-947-81

Alignment Scores:
  Pred. No.: 3,95e-53      Length: 5734
  Score: 547.50           Matches: 145
  Percent Similarity: 28.2% Conservative: 11
  Best Local Similarity: 26.2% Mismatches: 27
  Query Match: 52.2%      Indels: 371
  DB: 8                   Gaps: 5

US-10-723-947-77 (1-187) x US-10-723-947-81 (1-5734)

QY 1 MetSerMetSerCysGlyLeuCysGlyAlaAsnAsnCysProArgLeuMetValSerPro 20
   |||||
Db 2589 ATGTCATGTCATGCGGTTGTGCGCGCAAGGACTGCCCGCACCACCATGATCTCGCCC 2648

QY 21 IleHisHisHisHisHisHisHisGlnGluHisGlnLeuCysGluTyrGlnPhePheAla 40
   |||||
Db 2649 GTT-----CTTCAGCATCAGGAACACACATCGCTGCGCGAGTACCAGTTCTTCACC 2699

QY 41 HisGlyAsnHisHisHisHisHisGlySerAlaAlaAspTyrProValProProPro 60
   |||||
Db 2700 CAAAGG---CACCACCACCACCACCACCGCGCGCGGCGACTACCCACCGCCACGCCA 2756

QY 61 ProAsp---AsnPheAspHisArgArgThrTrpThrArgProPheHisGluThrAlaAla 79
   |||||
Db 2757 CCGTCGCGCAATTGCCACCACCTCCAGCATCATGAGCACCACACCGCTTCATGAAACAGCAGCT 2816

QY 80 AlaGlyAsnSerSerArgLeuThrLeuGluValGlyAlaGlyGlyGlnHisMetAlaHis 99
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Db 2817 GCAGGGAACAGACGACAGATCAGCTGGAGTAGATGACGCGCGGCCCAAAACATGGCTCAC 2876

QY 100 LeuValGlnProProAlaArg----- 106
   |||||
Db 2877 CTGCTGACGCCACCGCACCGCAAGAACACCACCATCGTGAGTAGTACTACTGCTTAATTG 2936

QY 106 ----- 106
Db 2937 TTCCAGCTCTTGCCGATCGCTGGGGCTCTCTTGTAACAAAAGTTCCCTTTTACGTAATCT 2996

QY 106 ----- 106
Db 2997 CCATCTACTCCCCCCCCCCCCCCCCCCCCCCCCCCCCCGCCGATCTCAAAAAAAGT 3056

QY 107 -----AlaHisIle----- 109
Db 3057 TAGCGCCATGTAACAGCTCATATATCTGTGCATATATCTGTGTAATTTATGCTGTCAA 3116

QY 109 ----- 109
Db 3117 TTATAATCTCCCAAGCAGAAAGTTGTGTTTGTATCATGTTGATGAACAAGAAATGGGAA 3176

QY 109 ----- 109
Db 3177 CTCACATCATCAGTTACACATACATATTTTATTTTATTTGACTAACAGGTAATCA 3236

QY 109 ----- 109
Db 3237 GTTAATTCCTTTTGGGAACAAGACATACATATGTCCAGCCTTCATGTTAATTCCTTCA 3296

QY 109 ----- 109
Db 3297 CAAAGTTTGTGAAATGGCAATATATATCTGGATCAATGACCCCTCTTTCTCATTTTAT 3356

QY 109 ----- 109
Db 3357 GTGGTCATTTATGAATTTTAGTGCTATTTATATTTTAAATTTTCTTCTTAAGCTTGTG 3416

QY 109 ----- 109
Db 3417 TAAGCTTATAGCTCATGTATATACAGATACACTCTCCCAATAATGTCTTCGTAGTGCGG 3476

QY 109 ----- 109
Db 3477 GTGATCAATCTACCGAGTTTATAAACTGATCGGGATCAGATCCAAAAACAGACAAACC 3536

QY 109 ----- 109
Db 3537 TCACGAAATAGAAAACAAGATCTCTTTTAAATTTGGCACCAGGAAATGCCACTACTTAA 3596

QY 109 ----- 109
Db 3597 TTACTTTCTATCAATCTTATGAACATGCGATGTTTCTCACATATGTTGACCCAGATCACA 3656

QY 109 ----- 109
Db 3657 ATTGTGACGAGTTAAACATTTTAGCAATTCATAAAACCATGCAAGATGTACAGGC 3716

QY 109 ----- 109
Db 3717 TAGCGTATGCACATACATATACACCTAATTTAAACATATATTTATAGAGCGATTGAGT 3776

QY 109 ----- 109
Db 3777 TTGGACTGTGCGCTTCTTTGGACACAAAGGCCCGGGAAGTTGTTCTTCTCCATTGTCTAG 3836

QY 109 ----- 109
Db 3837 AAAAATAGAACAGTTACAACTCAAGTGCACCACTGAATGAAAATGGGTCAACTCTGGTTAA 3896

QY 109 ----- 109
Db 3897 TAAGAGACCACTGTACTTTCATAAACAGAGGAATATCATGTACATATCTGCAACCCACAG 3956

QY 110 -----ValProPheTyr 113
Db 3957 AAAAGTACAGAGCTGCACCTTTTACAGTTATTTTCTCTTTCATGTTTCAGGTGCCATTCTGC 4016

QY 114 GlyGlyAlaPheThrAsnThrIleSerAsnGluAlaIleMetThrIleAspThrGluMet 133
   |||||
Db 4017 GGGGCTGCTATTCACCGACACTATTAGCAATGCAACATCATGACTATTGATACAGAGATG 4076

QY 134 MetValGlyProAlaHisTyrProThrMetGlnGluArgAlaAlaLysValMetArgTyr 153
   |||||
Db 4077 ATGGTGGGGCTGCCAATCTGACGATGACAGGAGAGAGCGGAGGATGATGAGTAC 4136

QY 154 ArgGlyLysArgLysArgArgTyrAspLysGlnIleArgTyrGluSerArgLysAla 173
   |||||
Db 4137 AGGGAGAAAGAGAGAGCGGCTGTATGACAGCAAAATCCGCTACGAGTCCAGAAAAGCT 4196

QY 174 TyrAlaGluLeuArgProArgValAsnGlyArgPheValLys 187
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Db 4197 TAGCCGAGCTCAGGCCCGGCTCAATGGCTCTTTGTCAAG 4238

RESULT 12
US-10-723-947-84
; Sequence 84, Application US/10723947
; Publication No. US20040205848A1
; GENERAL INFORMATION:
; APPLICANT: Dubcovsky, Jorge
; APPLICANT: Yan, Liuling
; APPLICANT: Loukoianov, Artem
; TITLE OF INVENTION: GENES RESPONSIBLE FOR VERNALIZATION
; TITLE OF INVENTION: REGULATION IN TEMPERATE GRASSES AND USES THEREOF
; FILE REFERENCE: 51411200320
; CURRENT APPLICATION NUMBER: US/10/723,947
; CURRENT FILING DATE: 2003-11-26
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; PRIOR APPLICATION NUMBER: US 10/412,137
; PRIOR FILING DATE: 2003-04-11
; NUMBER OF SEQ ID NOS: 159
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 84
; LENGTH: 3454
; TYPE: DNA
; ORGANISM: Triticum dicoccoides
US-10-723-947-84

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Score: 538.00 Matches: 145
Percent Similarity: 28.5% Conservative: 12
Best Local Similarity: 26.4% Mismatches: 26
Query Match: 51.3% Indels: 367
DB: 8 Gaps: 5

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QY 21 IleHisHisHisHisHisHisHisGlnGluHisGlnLeuCysGluTyrGlnPheAla 40
DB 1303 GTT-----CTTCAGCATCAGGAACACACCGGCTGGCGAGTACCAGTTCTTTCACC 1353
QY 41 HisGlyAsnHisHisHisHisHisHisGlySerAlaAlaAspTyrProValProPro 60
DB 1354 CAAGGC---CACCCACCACACACACGAGCGGCGGCGGACTACCACCGCCACGCCCA 1410
QY 61 ProAsp---AsnPheAspHisArgThrTriThrArgProPheHisGluThrAlaAla 79
DB 1411 CCGTCAGCCATTGCCACCACTCCAGATCATGACACACCGTTTCATGAACAGCAGCT 1470
QY 80 AlaGlyAsnSerSerArgLeuThrLeuGluValGlyAlaGlyGlyGlnHisMetAlaHis 99
DB 1471 GCAGGGAACAGCAGCAGGCTCAGCTGGAGGTAGACGCGCGCCAAACATGGCTCAC 1530
QY 100 LeuValGlnProProAlaArg----- 106
DB 1531 CTGCTGACGCCACCGGACGCGCCAGAACACCACCATCGTGAGTAGTACTACTGCTTAATG 1590
QY 106----- 106
DB 1591 TTCCAGCTCTTGGCGATCGCTTGGCGCTCCTCTTAACAAAAGTTCCCTTTTACGTAATCT 1650
QY 106----- 106
DB 1651 CCATCTACTCCCCCCCCCCCCCCCCCGGCATCTCAAAAAAAGTTAGCGCCATGTAACC 1710
QY 107 -AlaHisIle----- 109
DB 1711 AGCTCATATATCTGTACGTAATCTGTTAATTATGCTGGTTGAATATAATCTCCCAAG 1770
QY 109----- 109
DB 1771 GCAGAGTGTGTGTTTGTGTCAGTTGATGACACAGAAGTGGGCACTCACATCATCAGTT 1830
QY 109----- 109
DB 1831 ACACATACATCTTAATTTTCAATTTTATTTGACTAACAAAGGTAATCAGTTAATCTCTTATG 1890
QY 109----- 109
DB 1891 GGAACAAGCAATACATATGTCCACGCTTCATGTTAATTCCTTGACAAAGTTTGTGAAT 1950
QY 109----- 109
DB 1951 GGACATATATATCTGGATCAGTGACCATCTTTTTCATTTTATGTGGTCATTTATGAA 2010
QY 109----- 109
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DB 2011 TTTTAGTGCTATTTTGTATTAAATTTTCTTCTTAAGCTTGTGTTTGAAGCTTATAGCTC 2070
QY 109----- 109
DB 2071 AAGTATAACAGATACTACTCTCCCAATAATTGCTTCGCTAGTGGCGGGTGATCAATCTACC 2130
QY 109----- 109
DB 2131 GAGTTTCAAAAACTGATCGAAATCAGATCCAAAAACAGACCAAAACCTCAGAAATAGAAA 2190
QY 109----- 109
DB 2191 CAAGATCCTTGTGTTAATTAGTTTGACACAGGAAATTTGCCTACTTAATTACTTTCTATCAA 2250
QY 109----- 109
DB 2251 TCTTATGAAGATGGTATGTTTCTCATATGTTGATCCAGATCACAATTTGTTGACGGAGT 2310
QY 109----- 109
DB 2311 TAAACATTTTAGCAATTCATAAAACCGTGACAGATGTACAGGGCTACGCGTATGCACA 2370
QY 109----- 109
DB 2371 TACATAATACACCTAATTAAACACATATATTCATAGAGCGATTGAGTTGGACTGTGCGCT 2430
QY 109----- 109
DB 2431 TCTTTGGACACAAAGGCCCGGGAAGTTGTTCTTCTTCCATTGTTCTAGAAAAATAGAACAGT 2490
QY 109----- 109
DB 2491 TACAATCAGTGCACCACTGAATGAAATGGGTCAATTCTGGTTAATAAGAGACCAACTG 2550
QY 109----- 109
DB 2551 TACTTCATAAACAGGGAATATCATGTATATCTGCAACCCACAGAAAAAGTACAGAACT 2610
QY 110-----ValProPheTyrGlyAlaPheTh 118
DB 2611 GCACCTTACGATTATTTTCTCTTCATGTTCCAGGTGCCATTCGCGGGCTGCATTTCAC 2670
QY 118 rAsnThrIleSerAsnGluAlaIleMetThrIleAspThrGluMetMetValGlyProAl 138
DB 2671 CAGCACTATTAGCAATGCAACGATCATGACTATTGATACAGAGATGATGGTGGGGCTGC 2730
QY 138 aHisTyrProThrMetGlnGluArgAlaAlaLysValMetArgTyrArgGluLysArgLy 158
DB 2731 CCATAATCTGAGATGCGAGGAGAGAGAGCGGAAGGTGATGAGGTACAGGAGAAAGAGAA 2790
QY 158 sArgArgArgTyrAspLysGlnIleArgTyrGluSerArgLysAlaTyrAlaGluLeuAr 178
DB 2791 GAGCGGTGCTATGACAGCAATCCGCTATCAGTCCAGAAAAGCTTACGCGAGCTCAG 2850
QY 178 gProArgValAsnGlyArgPheValLys 187
DB 2851 GCCACGGGTCAATGGCGCTTTGTCAAG 2878
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## RESULT 13

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US-10-437-963-83163
; Sequence 83163, Application US/10437963
; Publication NO. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
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GenCore version 5.1.7  
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Run on: February 23, 2006, 10:42:28 ; Search time 183 Seconds  
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Title: US-10-723-947-77

Perfect score: 1048

Sequence: 1 MSMSGCLGCGANNCPRLMVSP.....YESRKAYAEALPRVNGRFVK 187

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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

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Listing first 45 summaries

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-NCPU=6 -ICPU=3 -NO MMAP -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents NA..\*

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2: /cgn2\_6/prodata/1/ina/5 COMB.seq.\*  
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4: /cgn2\_6/prodata/1/ina/6B COMB.seq.\*  
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6: /cgn2\_6/prodata/1/ina/6CTUS COMB.seq.\*  
7: /cgn2\_6/prodata/1/ina/PP COMB.seq.\*  
8: /cgn2\_6/prodata/1/ina/RE COMB.seq.\*  
9: /cgn2\_6/prodata/1/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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2	180.5	17.2	1101	3	US-08-945-056-5
3	175	16.7	1124	3	US-08-945-056-1
4	170	16.2	4201	3	US-08-945-056-4
5	161	15.4	448	3	US-09-640-211A-327
6	132	12.6	72549	3	US-09-949-016-16477
7	130	12.4	25603	3	US-09-819-607-3
8	129	12.3	39154	3	US-09-949-016-12384
9	129	12.3	39154	3	US-09-949-016-12801

c 10	129	12.3	39443	3	US-09-949-016-14326	Sequence 14326, A
c 11	129	12.3	39443	3	US-09-949-016-14327	Sequence 14327, A
c 12	127.5	12.2	67620	3	US-09-949-016-18939	Sequence 16939, A
c 13	126.5	12.1	152132	3	US-09-949-016-13845	Sequence 13845, A
c 14	126.5	12.1	152145	3	US-09-949-016-12371	Sequence 12371, A
c 15	126	12.0	55195	3	US-09-949-016-15854	Sequence 15854, A
c 16	126	12.0	142783	3	US-09-949-016-15127	Sequence 15127, A
c 17	124.5	11.9	18596	3	US-09-318-448-11	Sequence 11, Appl
c 18	124.5	11.9	18596	3	US-09-577-266-11	Sequence 11, Appl
c 19	124.5	11.9	18597	3	US-09-962-665-8	Sequence 8, Appl
c 20	124.5	11.9	18597	3	US-09-963-333-8	Sequence 8, Appl
c 21	124.5	11.9	18597	3	US-09-962-677-8	Sequence 20, Appl
c 22	123.5	11.8	3563	3	US-09-041-886-20	Sequence 20, Appl
c 23	123.5	11.8	3596	2	US-08-779-801-5	Sequence 5, Appl
c 24	123.5	11.8	3596	2	US-09-298-441-5	Sequence 5, Appl
c 25	123.5	11.8	3632	2	US-08-779-801-3	Sequence 3, Appl
c 26	123.5	11.8	3632	2	US-08-779-801-4	Sequence 4, Appl
c 27	123.5	11.8	3632	2	US-09-298-441-3	Sequence 3, Appl
c 28	123.5	11.8	3632	2	US-09-298-441-4	Sequence 4, Appl
c 29	123.5	11.8	7808	2	US-08-149-097D-22	Sequence 22, Appl
c 30	123.5	11.8	7808	3	US-08-949-386-22	Sequence 22, Appl
c 31	123.5	11.8	7808	3	US-08-450-562-22	Sequence 22, Appl
c 32	123.5	11.8	7808	3	US-08-984-709A-22	Sequence 22, Appl
c 33	123.5	11.8	7808	3	US-08-450-272-22	Sequence 22, Appl
c 34	123.5	11.8	7808	3	US-08-450-273-22	Sequence 22, Appl
c 35	123.5	11.8	7815	3	US-09-949-016-3629	Sequence 3629, Ap
c 36	123.5	11.8	7815	3	US-09-949-016-3630	Sequence 3630, Ap
c 37	123.5	11.8	34230	3	US-09-949-016-12052	Sequence 12052, A
c 38	123.5	11.8	128470	3	US-09-949-016-13765	Sequence 13765, A
c 39	122.5	11.7	840	3	US-09-248-796A-4756	Sequence 4756, Ap
c 40	121.5	11.6	1853	2	US-08-553-110-2	Sequence 2, Appl
c 41	121.5	11.6	4168	3	US-09-266-225D-17	Sequence 17, Appl
c 42	121.5	11.6	4279	3	US-09-041-886-22	Sequence 22, Appl
c 43	121	11.5	209	3	US-09-513-999C-14394	Sequence 14394, A
c 44	120.5	11.5	3680	2	US-08-759-848-1	Sequence 1, Appl
c 45	120.5	11.5	3680	6	PCT-US95-09383-1	Sequence 1, Appl

#### ALIGNMENTS

#### RESULT 1

US-08-945-056-7  
; Sequence 7, Application US/08945056  
; Patent No. 6077994  
; GENERAL INFORMATION:  
; APPLICANT: Coupland, George M.  
; APPLICANT: Putterill, Joanna J.  
; TITLE OF INVENTION: Genetic control of flowering  
; NUMBER OF SEQUENCES: 31  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Nixon & Vanderhye PC  
; STREET: 8th Floor, 1100 No. 6077994th Glebe Road  
; CITY: Arlington  
; STATE: Virginia  
; COUNTRY: United States of America  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/945,056  
; FILING DATE: 20-OCT-1997  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/GB95/02561  
; FILING DATE: 01-NOV-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 9422083.7  
; FILING DATE: 02-NOV-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ms Mary J Wilbon  
; REGISTRATION NUMBER: 32,955



Db 682 ATCACTATGGCTCTCCAGCAATGCTTCAACCAACATGGTTCCATAAACCATACGCA 741  
QY 101 ValGlnProAlaArgAlaHisIleValProPheTyrGlyGlyAlaPheThrAsnThr 120  
Db 742 TACAATCCATCAATGGAAGTGAAGTCTTGTTCGCG--GAGCAGACAGCACTGACAAACA 798  
QY 121 IleSerAsnGluAlaIleMetThrIleAspThrGluMetMetValGlyPro--AlaHis 139  
Db 799 GTTTCATCTCCAAAACGCAAGGAGATAGAAAACCTGCTGAACCTCTAATTCAG 858  
QY 140 TyrProMetGlnGluArgAlaAlaLysValMetArgTyrArgGluLysArgLysArg 159  
Db 859 ATTCTCAGTCCATGACAGAGAGCTAGAGCTCTGATACAGAGAGAGAGAGAGA 918  
QY 160 ArgArgTyrAspLysGlnIleArgTyrGluSerArgLysAlaTyrAlaGluLeuArgPro 179  
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QY 180 ArgValAsnGlyArgPheValLys 187  
Db 979 AGGATCAATGGACGGTTTCAAG 1002

## RESULT 3

US-08-945-056-1  
; Sequence 1, Application US/08945056  
; Patent No. 6077994  
; GENERAL INFORMATION:  
; APPLICANT: Coupland, George M.  
; APPLICANT: Putterill, Joanna J.  
; TITLE OF INVENTION: Genetic control of flowering  
; NUMBER OF SEQUENCES: 31  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Nixon & Vanderhye PC  
; STREET: 8th Floor, 1100 No. 6077994th Glebe Road  
; CITY: Arlington  
; STATE: Virginia  
; COUNTRY: United States of America  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/945,056  
; FILING DATE: 20-OCT-1997  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/GB95/02561  
; FILING DATE: 01-NOV-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 9422083.7  
; FILING DATE: 02-NOV-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ms Mary J Wilson  
; REGISTRATION NUMBER: 32,955  
; REFERENCE/DOCKET NUMBER: 620-17  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703) 816-4000  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1124 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA to mRNA  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; ORIGINAL SOURCE:  
; ORGANISM: Arabidopsis thaliana  
; STRAIN: Landsberg erecta  
; POSITION IN GENOME:  
; CHROMOSOME/SEGMENT: chromosome 5

FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..1119  
; US-08-945-056-1  
Alignment Scores:  
Pred. No.: 1.82e-08 Length: 1124  
Score: 175.00 Matches: 51  
Percent Similarity: 40.9% Conservative: 25  
Best Local Similarity: 27.4% Mismatches: 56  
Query Match: 16.7% Indels: 54  
DB: 3 Gaps: 5

US-10-723-947-77 (1-187) x US-08-945-056-1 (1-1124)

QY 9 GlyAlaAsnAsnCyProArgLeuMetValSerProIleHisHisHisHisHisHis 28  
Db 625 GGGGAGATAGAGTGTTCCTTAACCTTGAAGGGAATCAAGGGGGCCACCAGTGCCTAAC 684  
QY 29 GlnGluHisGlnLeuCysGluTyrGlnPheAlaHisGlyAsnHisHisHisHis 45  
Db 685 CAACAGAATTTTCAGTTCAATATCAATATGCTCTCAGGGAGCTCCTACACGCAAT 744  
QY 46 -----HisHisHisGlySerAlaAlaAspTyrProValProProPro 61  
Db 745 GTTTCATTAACCATACGATACATATTCATCCAGAACTGGTGTGTGCGG----- 798  
QY 62 AspAsnPheAspHisArgArgThrTrpThrArgProPheHisGluThrAlaAlaGly 81  
Db 799 -----GAGTCAACAGCATGTGTGCACA 819  
QY 82 AsnSerSerArgLeuThrLeuGluValGlyAlaGlyGlyGlnHisMetAlaHisLeuVal 101  
Db 820 ACAGCTTTCACACCCCAAGAACGCCCAAGGAGCAGTAGAGCAA----- 861  
QY 102 GlnProProAlaArgAlaHisIleValProPheTyrGlyGlyAlaPheThrAsnThrIle 121  
Db 862 CAACCTGACCTCGCAAGCCAGATGATA----- 888  
QY 122 SerAsnGluAlaIleMetThrIleAspThrGluMetMetValGlyProAlaHisTyrPro 141  
Db 889 -----ACAGTAACACAACTCAGTCCA----- 909  
QY 142 ThrMetGlnGluArgAlaAlaLysValMetArgTyrArgGluLysArgLysArgArg 161  
Db 910 -----ATGGACAGAGAAGCCAGGGTCTCTGAGATACAGAGAAGAGGAGCAAGGAAA 963  
QY 162 TyrAspLysGlnIleArgTyrGluSerArgLysAlaTyrAlaGluLeuArgProArgVal 181  
Db 964 TTTGAGAGACATAAGGTATGCTTCGAGGAAGGCATATGACAGAGATAAGCCGGGTC 1023  
QY 182 AsnGlyArgPheValLys 187  
Db 1024 AATGGCCGGTTTCGCAAG 1041

## RESULT 4

US-08-945-056-4  
; Sequence 4, Application US/08945056  
; Patent No. 6077994  
; GENERAL INFORMATION:  
; APPLICANT: Coupland, George M.  
; APPLICANT: Putterill, Joanna J.  
; TITLE OF INVENTION: Genetic control of flowering  
; NUMBER OF SEQUENCES: 31  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Nixon & Vanderhye PC  
; STREET: 8th Floor, 1100 No. 6077994th Glebe Road  
; CITY: Arlington  
; STATE: Virginia  
; COUNTRY: United States of America  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible











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; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15854
; LENGTH: 55195
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-15854

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Alignment Scores:
Pred. No.: 0.363 Length: 55195
Score: 126.00 Matches: 21
Percent Similarity: 61.5% Conservative: 3
Best Local Similarity: 53.8% Mismatches: 14
Query Match: 12.0% Indels: 2
DB: 3 Gaps: 1

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US-10-723-947-77 (1-187) x US-09-949-016-15854 (1-55195)

```

Qy 22 HisHisHisHisHisHisHisHisGlnGlnHisGlnLeuCysGluTyxClnPhePheAlaHis 41
Db 49369 CATCACCCACCACCACCACCACCACCACCACCACCATTACTGTC---CATCAACATCACCATCAC 49425
Qy 42 GlyAsnHisHisHisHisHisHisGlySerAlaAlaAspTyxProValProProPro 60
Db 49426 CATCATCACCCACCACCACCATTATCAACCATCATCACCACCATT-CCACCACCA 49481

```

Search completed: February 23, 2006, 12:01:53  
Job time : 221 secs

GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: February 23, 2006, 10:39:32 ; Search time 3661 Seconds

(without alignments)  
2389.835 Million cell updates/sec

Title: US-10-723-947-77

Perfect score: 1048

Sequence: 1 MMSCLCGANNCPLMVSP.....YESRKAYAEPRVNGRFVK 187

Scoring table:

BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlh  
-O=/abes/ABSSWEB.spool/US10723947/runat.23022006.085359.16224/app.query.fasta\_1  
-DB=EST -OFMT=fastap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=pro -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abs02h  
-USER=US10723947 @CGN 1.1 5315 @runat.23022006.085359.16224 -NCPU=6 -ICPU=3  
-NO MMAP -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120  
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7  
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

EST:\*\*

1: gb\_est1:\*  
2: gb\_est2:\*  
3: gb\_est3:\*  
4: gb\_est4:\*  
5: gb\_est5:\*  
6: gb\_est6:\*  
7: gb\_est7:\*  
8: gb\_est8:\*  
9: gb\_gss1:\*  
10: gb\_gss2:\*  
11: gb\_gss3:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	253	24.1	864	10	CL972569 OsIFCC023
2	219	20.9	689	8	DN238319 MUC4LH100
3	213	20.3	1305	4	EX811971 Arabidops
4	209	19.9	848	7	CV291360 acof01-5ms
5	207	19.8	815	8	DR750621 48-L02059
6	207	19.8	817	8	DN604709 JCAT5g576
7	207	19.8	829	5	BU636028 044E12 In

8	207	19.8	1308	4	CNS0925B
9	207	19.8	1335	4	CNS091N5
10	205	19.6	563	6	CB911506
11	205	19.6	596	6	CD007533
12	205	19.6	631	6	CD010195
13	205	19.6	650	6	CD010575
14	205	19.6	712	3	BM436387
15	204.5	19.5	546	10	CZ787328 OC_Ba015
16	204	19.5	548	2	BI074743 IFI_15_F0
17	204	19.5	626	6	CD010039
18	203	19.4	761	9	CC728227 OGCV57TM
19	203	19.4	780	8	DR9310452
20	201	19.2	850	9	CC685007
21	201	19.2	907	9	CC885002
22	199	19.0	822	7	CK275343
23	199	19.0	851	7	CK274891
24	197	18.8	519	7	CV545348
25	197	18.8	582	1	AI488780
26	195.5	18.7	843	5	BO797187
27	195	18.6	536	3	BM528344
28	195	18.6	549	5	BU084004
29	195	18.6	577	3	BM271055
30	195	18.6	579	3	BQ299156
31	195	18.6	587	5	BU081045
32	195	18.6	634	8	CX538017
33	195	18.6	742	6	CA919328
34	195	18.6	780	7	CK248987
35	194.5	18.6	564	5	BQ588069
36	194.5	18.6	622	7	CV458983
37	194.5	18.6	833	9	BZ734187
38	194	18.5	678	6	CA800072
39	194	18.5	723	7	CK255880
40	194	18.5	815	7	CK279398
41	194	18.5	820	7	CK245114
42	193.5	18.5	1021	10	CL012630
43	192	18.3	640	10	CL925503
44	192	18.3	661	6	CB003731
45	192	18.3	668	6	CB001303

#### ALIGNMENTS

RESULT 1

CL972569

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

CL972569 864 bp DNA linear GSS 21-SEP-2004  
OsIFCC023161 Oryza sativa Express Library Oryza sativa (indica  
cultivar-group) genomic, genomic survey sequence.

CL972569.1 GI:52399671

GSS.

Oryza sativa (indica cultivar-group)

Oryza sativa (indica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 864)

Ma, L., Wang, J., Chen, C., Liu, X., Su, N., Li, L., Wang, X., Cao, M.,

Jiao, Y., Sun, N., Zhang, X., Bao, J., Sun, D., Zhao, H., Yuan, L.,

Wong, G.K.S., Deng, X.W. and Wang, J.

An analysis of transcriptional regulation of the rice genome and

its comparison to Arabidopsis

Unpublished (2004)

Contact: Chen Chen

Department of Bioinformatics

Beijing Institute of Genomics

Chinese Academy of Sciences, Beijing 101300, China

Tel: 86-10-80481559

Fax: 86-10-80488676

Email: chenchen@genomics.org.cn

Rice genomic sequence.

Class: exon-trapped.

Location/Qualifiers

1..864

source





```

LOCUS       CV291360               848 bp    mRNA       linear       EST 09-JUN-2005.
DEFINITION   aof01-5msl-b04 Aof01 Asparagus officinalis cDNA clone
aof01-5msl-b04 5', mRNA sequence.
ACCESSION    CV291360
VERSION      CV291360.1 GI:52577578
KEYWORDS     EST.
SOURCE       Asparagus officinalis (garden asparagus)
ORGANISM     Asparagus officinalis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta, Liliopsida; Asparagales;
Asparagaceae; Asparagus.
1 (bases 1 to 848)
dePamphilis,C., Carlson,J., Ma,H., Soltis,D., Soltis,P.,
Oppenheimer,D., Frohlich,M., Doyle,J., Tanksley,S., Webb,M.,
Leebens-Mack,J., Landherr,L., Flut,D. and Wall,K.
Generation of ESTs from early male inflorescences of Asparagus
officinalis
Unpublished (2004)
Contact: Claude dePamphilis or James Leebens-Mack
Mueller Laboratory
Penn State University
208 Mueller Laboratory, Department of Biology, ATTN Rm212, Penn
State University, University Park, PA 16802, USA
Tel: 814 863 6413
Fax: 814 865 9131
Email: cws3@psu.edu or jhl10@psu.edu
The sequence provided is trimmed of vector and low quality regions.
Full sequence and original trace file are available from the Plant
Genome Network website (http://pgn.cornell.edu)
Plate: aof01-5msl row: b column: 04
Seq primer: M13F.
Location/Qualifiers
1..848
/organism="Asparagus officinalis"
/mol_type="mRNA"
/db_xref="PGN:aof01-5msl-b04"
/db_xref="taxon:4686"
/clone="aof01-5msl-b04"
/tissue_type="male inflorescences"
/lab_host="SOLR"
/clone_lib="Aof01"
/notes="Vector: pBluescript SK (+/-); Site 1: EcoRI;
Site 2: XhoI; this is a directionally cloned,
non-normalized library. This library has been generated by
the Floral Genome Project (FGP). The Floral Genome Project
is funded by NSF's Plant Genome Research Program
(DBI-0115684). More information about the project can be
obtained at http://fgp.bio.psu.edu"

ALIGNMENT SCORES:
Pred. No.:      5,48e-10      Length:      848
Score:          209.00      Matches:     65
Percent Similarity: 40.9%      Conservative: 23
Best Local Similarity: 30.2%      Mismatches:  81
Query Match:    19.9%      Indels:     46
DB:             7           Gaps:       6

US-10-723-947-77 (1-187) x CV291360 (1-848)
Qy      6 GlyLeuCyGlyAlaAenCysProArGLeuMetValSerProLeHisHisHis 25
|||
Db      2 GGCCAAACCTCAAGCAATGCTTCCTCACTGTATCGCGCTCAACCGCGCGTAGCG 61
|||
Qy      26 HisHisHisGlnGluHisGlnLeuCyGlyTyrGlnPheAlaHisGlyAsnHisHis 45
|||
Db      62 GGCCACGCGCGGCTCAAGCGCTTCAGGAGTTCCTCAATCTTTCCAAAGGACACGTTG 121
|||
Qy      46 HisHisHisGlySerAlaAlaAspTyrProValProProProAspAsnPheAsp 65
|||
Db      122 GCGTGGCTGTTTAATCACTCAAGCGCGCGCGCGGCGGCAACAGGCGCTGAGGATC--- 178
|||
Qy      66 HisArgArgThrTrpThrArgProPheHisGluThrAlaAlaGly----- 81
|||

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LOCUS       DR750621/c            815 bp    mRNA       linear       EST 19-JUL-2005
DEFINITION   48-L020593-065-004-H06-SELB MP1Z-ADIS-065d Arabidopsis thaliana
CDNA clone 004-H06, mRNA sequence.
ACCESSION    DR750621
VERSION      DR750621.1 GI:71035961
KEYWORDS     EST.
SOURCE       Arabidopsis thaliana (thale cress)
ORGANISM     Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
1 (bases 1 to 815)
Paz-Ares,J., Valencia,A., Costantino,P., Vittorioso,P., Davies,B.,
Gilmartin,P., Giraudat,J., Parcy,F., Reindl,A., Sablowski,R.,
Coupland,G., Martin,C., Angenent,G.C., Baumelein,H., Mock,H.P.,
Carbonero,P., Colombo,L., Tonelli,C., Engstrom,P.,
Droegge-Laser,W., Gatz,C., Kavanagh,T., Kushnir,S., Zabeau,M.,
Laux,T., Hordsworth,M., Ruberti,I., Ratcliff,F., Smeekens,S.,
Somesich,I., Weishaar,B. and Traas,J.
REGIA, an EU project on functional genomics of transcription
factors from Arabidopsis thaliana
Comp. Funct. Genomics 3 (2), 102-108 (2002)
Contact:
Paz-Ares, Costantino, Vittorioso, Davies, Gilmartin, Giraudat, Parcy, Sablowski,
Coupland, Martin, Angenent, Baumelein, Carbonero, Colombo, Tonelli,
Engstrom, Droegge-Laser, Gatz, Kavanagh, Kushnir, Zabeau, Laux, Hordsworth,
Ruberti, Smeekens, Somesich, Weishaar, Traas
Bielefeld University, Institute for Genome Research
Universitaetstrasse 25, D-33594 Bielefeld, Germany
Email: bernd.weishaar@uni-bielefeld.de
AGI: A75G57660; SeqAnalysis: full CDS correct; Translation: full
good
Data analysis performed in the frame of REGULATORS (Exploiting
inter-species conservation in promoter sequences to identify
regulators of reproductive development and physiological
performance), a Trilateral Co-Operation in Plant Genomics between
Spain (MCYT), France (GENOPLANTE) and Germany (GABI) coordinated by
G. Coupland (coupland-ad-mpiz-koeln.mpg.de). Authors: Vincent
Thureau (IBP-Orsay UMR8618 CNRS-UPS, thureau-ad-ibp.u-psud.fr) and
Alain Lecharny (URGV-Evry UMR INRA-CNRS-UEVE,

```

---

```

RESULT 5
DR750621/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

```





Alignment Scores:		Location/Qualifiers	
Pred. No.:	8.19e-10	1..829	
Score:	207.00	/organism="Arabidopsis thaliana"	
Percent Similarity:	47.4%	/mol_type="mRNA"	
Best Local Similarity:	32.2%	/ecotype="Columbia"	
Query Match:	19.8%	/db_xref="taxon:3702"	
DB:	8	/dev_stage="Plant 3 weeks old, three days post infection"	
		/clone_lib="Infected Arabidopsis Leaf"	
		/note="Organ: Leaf; Vector: pBluescript; Mixed cDNA library of Arabidopsis and E. cichoracearum infected leaf from three weeks old Arabidopsis plants. Plants were harvested 3 days after infection and mRNA oligo dT selected."	
US-10-723-947-77 (1-187) x DN604709 (1-817)			
QY	32	GlnLeuCysGluTyrGlnPhePheAlaHisGlyAsnHisHisHisHisHisGlySer	51
DB	526	CGGCTTATTGATTCGAGTTCCGAATTCGTTCAATCATCAAAACACGCCGAGGA	467
QY	52	AlaAlaAspTyrProVal	66
DB	466	GATAGTCTTGTTCGGTTTCAGAGAAACAGAGCCTCTCCGTTAACTAATCATGATCAT	407
QY	67	ArgArgThrThrArgProPheHisGlu	76
DB	406	TGCTTCGATATTGATTTCTGCAGATCAAAAGCTCTCTGCTTTCACCTTACCTTCAATCA	347
QY	77	ThrAlaAlaAlaGlyAsnSerArgLeuThrLeuGluValGlyAlaGlyGlnHis	96
DB	346	GTCCAGCCACAGTGTTCGACTTCT	308
QY	97	MetAlaHisLeuValGlnProProAlaArgAlaHisIleValProPheTyrGlyGlyAla	116
DB	307	GTAGTTCTCT	290
QY	117	PheThrAsnThrIleSerAsnGluAlaIleMetThrIleAspThrGluMetValGly	136
DB	289	ACAAACAACCTCTGTTAAACCGAGCAGATC	242
QY	137	ProAlaHisIleProThrMetGlnGluArgAlaAlaLysValMetArgTyrArgGluLys	156
DB	241	GGTGATCATCAACGAGCTCTTGGATAGAGAGCTAGGTTTGGAGGTACAGAGAGAG	182
QY	157	ArgLysArgArgTyrAspLysGlnIleArgTyrGluSerArgLysAlaTyrAlaGlu	176
DB	181	AGAAAGACAGGAAATTTGAGAGAGAGATTCGTACGCTTCGAGGAAGCTTATGCAGAG	122
QY	177	LeuArgProArgValAsnGlyArgPheValLys	187
DB	121	TCACGCCCAAGGATCAAAAGCGGTTTGCAGAA	89
RESULT 7			
BU636028			
LOCUS			
DEFINITION			
044812 Infected Arabidopsis Leaf Arabidopsis thaliana cdna, mRNA			
sequence.			
*ACCESSION			
BU636028			
VERSION			
BU636028.1 GI:23303283			
KEYWORDS			
Arabidopsis thaliana (thale cress)			
SOURCE			
ORGANISM			
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta;			
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;			
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.			
1 (bases 1 to 829)			
Lundsgaard M., Emmersen, J., Nielsen, K.L., Wilson, I., Somerville, S.			
and Welinder, K.G.			
EST sequencing of Erysiphe cichoracearum infected Arabidopsis			
plants			
Unpublished (2002)			
Contact: Karen G. Welinder			
Institut for bioteknologi			
Aalborg Universitet			
Sohngaardsholmsvej 49, 9000 Aalborg, Denmark			
Tel: +45 96358467			
Fax: +45 98141808			
Email: kgw@bio.au.dk.			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
COMMENT			
FEATURES			
source			
ORIGIN			
Alignment Scores:			
Pred. No.:	8.35e-10	Length:	829
Score:	207.00	Matches:	55
Percent Similarity:	47.4%	Conservative:	26
Best Local Similarity:	32.2%	Mismatches:	50
Query Match:	19.8%	Indels:	40
DB:	5	Gaps:	6
US-10-723-947-77 (1-187) x BU636028 (1-829)			
QY	32	GlnLeuCysGluTyrGlnPhePheAlaHisGlyAsnHisHisHisHisHisGlySer	51
DB	288	CGGCTTATTGATTTCCGAATTCGTTCAATCATCAAAACACGCCGAGGA	347
QY	52	AlaAlaAspTyrProVal	66
DB	348	GATAGTCTTGTTCGGTTTCAGAGAAACAGAGCCTCTCCGTTAACTAATCATGATCAT	407
QY	67	ArgArgThrThrArgProPheHisGlu	76
DB	408	TGCTTCGATATTGATTTCTGCAGATCAAAAGCTCTCTGCTTTCACCTTCAATCA	467
QY	77	ThrAlaAlaAlaGlyAsnSerArgLeuThrLeuGluValGlyAlaGlyGlnHis	96
DB	468	GTCCAGCCACAGTGTTCGACTTCT	506
QY	97	MetAlaHisLeuValGlnProProAlaArgAlaHisIleValProPheTyrGlyGlyAla	116
DB	507	GTAGTTCTCT	524
QY	117	PheThrAsnThrIleSerAsnGluAlaIleMetThrIleAspThrGluMetValGly	136
DB	525	ACAAACAACCTCTGTTAAACCGAGCAGATC	572
QY	137	ProAlaHisIleProThrMetGlnGluArgAlaAlaLysValMetArgTyrArgGluLys	156
DB	573	GGTGTATCATCAAGCGAGCTCTATGTAGAGAGAGCTAGGTTTGGAGGTACAGAGAGAG	632
QY	157	ArgLysArgArgTyrAspLysGlnIleArgTyrGluSerArgLysAlaTyrAlaGlu	176
DB	633	AGAAAGACAGGAAATTTGAGAGAGAGATTCGTACGCTTCGAGGAAGCTTATGCAGAG	692
QY	177	LeuArgProArgValAsnGlyArgPheValLys	187
DB	693	TCACGCCCAAGGATCAAAAGCGGTTTGCAGAA	725
RESULT 8			
CNS09ZSB			
LOCUS			
DEFINITION			
Arabidopsis thaliana Full-length cDNA Complete sequence from clone			
GSLTPGH12B11 of Hormone Treated Callus of strain col-0 of			
Arabidopsis thaliana (thale cress).			
BX831501			
BX831501.1 GI:42456535			
KEYWORDS			
Arabidopsis thaliana (thale cress)			
SOURCE			
ORGANISM			
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta;			
CNS09ZSB			
1308 bp mRNA linear HTC 06-FEB-2004			

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE 1 (bases 1 to 1308)

AUTHORS Castelli,V., Aury,J.M., Jaillon,O., Wincker,P., Clepet,C., Menard,M., Cruaud,C., Quetier,F., Scarpelli,C., Schachter,V., Temple,G., Caboche,M., Weissenbach,J. and Salanoubat,M.

TITLE Whole Genome Sequence Comparisons and 'Full-length' cDNA Sequences: A Combined Approach to Evaluate and Improve Arabidopsis Genome Annotation

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 1308)

AUTHORS Genoscope.

TITLE Direct Submission

JOURNAL Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)

COMMENT The sequences are based on single pass reads. Life Technologies (a division of Invitrogen) members carried out full-length libraries construction : Temple G. Genoscope members carried out sequencing and annotation : Castelli V., Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C., Schachter V., Weissenbach J., Salanoubat M. URGV INRA : Clepet C., Caboche M. Annotation is based on the June 2003 version of the Arabidopsis genome released by MIPS (Munich Information center for Protein Sequences). 5 prime and 3 prime are assembled with Phrap. [http://www.genoscope.cns.fr/externe/sequences/Banque\\_Projet\\_EF/Full\\_length](http://www.genoscope.cns.fr/externe/sequences/Banque_Projet_EF/Full_length)

FEATURES

Location/Qualifiers

1..1308

/organism="Arabidopsis thaliana"

/mol\_type="mRNA"

/db\_xref="taxon:3702"

/clone="GSLTPGH12H1"

/tissue\_type="Hormone Treated Callus"

/ecotype="Col-0"

/plasmid="pCMVSPORT\_6"

1..1308

/gene="At5g57660"

gene

ORIGIN

Alignment Scores:

Pred. No.: 1..51e-09 Length: 1308

Score: 207.00 Matches: 55

Percent Similarity: 47.4% Conservative: 26

Best Local Similarity: 32.2% Mismatches: 50

Query Match: 19.8% Indels: 40

DB: 4 Gaps: 6

US-10-723-947-77 (1-187) x CNS092SB (1-1308)

QY 32 GlnLeuCysGlyThrGlnPheAlaHisGlyAsnHisHisHisHisHisGlySer 51

DB 579 CGCGTTATTGATTTCGAGTTTCGGAATTCGTTCAATCATCATCAAAACAACCGCGAGCA 638

QY 52 AlaAlaAspTyrProVal-----ProProProProAspAsnProAspHis 66

DB 639 GATAGTCTTTGTTCCCGGTTTCAGACGAAACAGAGCCTCTCCCGTTAACTAACAAATGATCAT 698

QY 67 -----ArgArgThrTrpThrArgProPheHisGlu 76

DB 699 TCGTTCGATTTGATTTTCGAGATCAAGCTCTGCTTTTACTTACCTTCTCAATCA 758

QY 77 ThrAlaAlaAlaGlyAsnSerArgLeuThrLeuGluValGlyAlaGlyGlyGlnHis 96

DB 759 GTCAGCCACAGTGTTCGACTTCT-----TCPTATTGAATACGTT----- 797

QY 97 MetAlaHisLeuValGlnProProAlaArgAlaHisIleValProPheTyrGlyGlyAla 116

DB 798 -----GTAGTTCTCT-----GACGGAAAC 815

QY 117 PheThrAsnThrIleSerAsnGluAlaIleMetThrIleAspThrGluMetMetValGly 136

816 ACAACAACACTGTTGTAACCGGAGCAGATC-----ACTAGCTCGACGACTGGT 863

QY 137 ProAlaHisTyrProThrMetGlnGluArgAlaAlaLysValMetArgTyrArgGluLys 156

DB 864 GGTGATCATCATCAAGCGAGCTCTTATGATGAGAGCTAGGTTTGTAGGTACAGAGAAG 923

QY 157 ArgLysArgArgTyrAspLysGlnIleAspTyrGluSerArgLysAlaTyrAlaGlu 176

DB 924 AGAAGAACACAGGAATTTGAGAAGAGGATTCGTTACGTTTCGAGGAAAGCTTATGCAGAG 983

QY 177 LeuArgProArgValAsnGlyArgPheValLys 187

DB 984 TCACGCCCAAGATCAAGGCGGTTTGCAGAA 1016

RESULT 9

CNS09YN5 1335 bp mRNA linear HTC 06-FEB-2004

LOCUS Arabidopsis thaliana Full-length cDNA Complete sequence from clone

DEFINITION GSLTPGH562A01 of Hormone Treated Callus of strain col-0 of Arabidopsis thaliana (thale cress).

ACCESSION EX832165

VERSION EX832165.1 GI:42455085

KEYWORDS HTC; GSLT cDNA.

SOURCE Arabidopsis thaliana (thale cress)

ORGANISM Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE 1 (bases 1 to 1335)

AUTHORS Castelli,V., Aury,J.M., Jaillon,O., Wincker,P., Clepet,C., Menard,M., Cruaud,C., Quetier,F., Scarpelli,C., Schachter,V., Temple,G., Caboche,M., Weissenbach,J. and Salanoubat,M.

TITLE Whole Genome Sequence Comparisons and 'Full-length' cDNA Sequences: A Combined Approach to Evaluate and Improve Arabidopsis Genome Annotation

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 1335)

AUTHORS Genoscope.

TITLE Direct Submission

JOURNAL Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)

COMMENT The sequences are based on single pass reads. Life Technologies (a division of Invitrogen) members carried out full-length libraries construction : Temple G. Genoscope members carried out sequencing and annotation : Castelli V., Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C., Schachter V., Weissenbach J., Salanoubat M. URGV INRA : Clepet C., Caboche M. Annotation is based on the June 2003 version of the Arabidopsis genome released by MIPS (Munich Information center for Protein Sequences). 5 prime and 3 prime are assembled with Phrap. [http://www.genoscope.cns.fr/externe/sequences/Banque\\_Projet\\_EF/Full\\_length](http://www.genoscope.cns.fr/externe/sequences/Banque_Projet_EF/Full_length)

FEATURES

Location/Qualifiers

1..1335

/organism="Arabidopsis thaliana"

/mol\_type="mRNA"

/db\_xref="taxon:3702"

/clone="GSLTPGH562A01"

/tissue\_type="Hormone Treated Callus"

/ecotype="Col-0"

/plasmid="pCMVSPORT\_6"

1..1335

/gene="At5g57660"

gene

ORIGIN

Alignment Scores:

Pred. No.: 1.55e-09 Length: 1335

Score: 207.00 Matches: 55

Percent Similarity: 47.4% Conservative: 26



Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
rosids; Vitaceae; Vitis.

## REFERENCE

1 (bases 1 to 596)

## AUTHORS

Cramer, G.R. and Cushman, J.C.

## TITLE

An expressed sequence tag database for abiotic stressed leaves of

## JOURNAL

Vitis vinifera var. Chardonnay

## COMMENT

Unpublished (2002)

Contact: Cushman JC

Department of Biochemistry

University of Nevada

MS200, Reno, NV 89557-0014, USA

Tel: 775-784-1918

Fax: 775-784-1650

Email: jcushman@unr.edu

PCR Primers

FORWARD: T3 20mer

BACKWARD: T7 21mer (backward)

Plate: 0 row: E column: 11

Seq primer: T3 20mer

High quality sequence stop: 596.

Location/Qualifiers

1..596

/organism="Vitis vinifera"

/mol\_type="mRNA"

/db\_xref="taxon:29760"

/clone="VVB072E11"

/tissue\_type="leaf"

/dev\_stage="juvenile and adult"

/clone\_lib="An expressed sequence tag database for abiotic

stressed leaves of Vitis vinifera var. Chardonnay"

/notes="Vector: Lambda Uni-Zap XR, Bluescript SK-; Site 1:

EcoRI; Site 2: XhoI; Library construction was performed

according to Stratagene's recommended protocol for the

Lambda UniZapXR vector and cDNA synthesis kit."

ORIGIN

Alignment Scores:

Pred. No.: 8 52e-10 Length: 596

Score: 205.00 Matches: 54

Percent Similarity: 46.3% Conservative: 21

Best Local Similarity: 33.3% Mismatches: 53

Query Match: 19.6% Indels: 34

DB: 6 Gaps: 5

US-10-723-947-77 (1-187) x CD007533 (1-596)

QY 44 HisHisHisHisHisHisGlySerAlaAlaAasp-----Tyr 55

DB 121 CACCATCATCACCACCACTGCGGTGGAATGATGTTCCGGTTCAGGCAAGAT 180

QY 56 ProValProPro-----ProProAspAsn-----PheAspHisArgArg 68

DB 181 CCCTCACCTCCGGTCAAGAACCAACCCCTGTCACAAATGTTTGAAGTGGATTTCTCTCGA 240

QY 69 ThrTrpThrArgProPheHisGluThrAlaAlaAlaGlyAsnSerSerArgLeuThrLeu 88

DB 241 TCAAGCTCTCGCTTACCACTATACAGCTCAATCTTAAGCCAAAGCATTTCTTCTCA 300

QY 89 GluValGlyAla-----GlyGlyGlnHisMetAlaHisLeuValGlnProProAla 105

DB 301 GATGTTGGGGTGTCCAGATGGGAAGTCACTCCATGCTGATACATCCCTACCTTCG 360

QY 106 ArgAlaHisIleValProPheThrGlyGlyAlaPheThrAsnThrIleSerAsnGluAla 125

DB 361 ATCAAGCAAGTCAAGCGGCGCGCGGGTCTTACTGGAGTCAAGCGACCAATTA 420

QY 126 IleMetThrIleAspThrGluMetMetValGlyProAlaHisThrProThrMetGlnGlu 145

DB 421 -----TCTGGAATGGAT 432

QY 146 ArgAlaAlaLysValMetArgTyrArgGlyLysArgArgArgArgTyrAspLysGln 165

DB 433 CGCGAAGCGGGTGTGTAGGTACAGAGAGAGAGAACCGGAAATTCGGAATACC 492

QY 166 lIcArgTyrGluSerArgLysAlaTyrAlaGluLeuArgProArgValaenGlyArgphe 185

DB 493 ATCAGATACGCTCCAGAAAGCCTACGCGAGACCGTCCAAAGATTCAGAGCCGCTTC 552

QY 186 Vallys 187

DB 553 GCAGAG 558

RESULT 12

CD010195 631 bp mRNA linear EST 02-MAY-2003

LOCUS VVB104H08 341909 An expressed sequence tag database for abiotic

stressed leaves of Vitis vinifera var. Chardonnay Vitis vinifera

CDNA clone VVB104H08 5, mRNA sequence.

ACCESSION CD010195

VERSION CD010195.1 GI:30326933

KEYWORDS EST.

SOURCE Vitis vinifera

ORGANISM Vitis vinifera

REFERENCE 1 (bases 1 to 631)

AUTHORS Cramer G.R. and Cushman, J.C.

TITLE An expressed sequence tag database for abiotic stressed leaves of

Vitis vinifera var. Chardonnay

JOURNAL Unpublished (2002)

COMMENT Contact: Cushman JC

Department of Biochemistry

University of Nevada

MS200, Reno, NV 89557-0014, USA

Tel: 775-784-1918

Fax: 775-784-1650

Email: jcushman@unr.edu

PCR Primers

FORWARD: T3 20mer

BACKWARD: T7 21mer (backward)

Plate: 1 row: H column: 08

Seq primer: T3 20mer

High quality sequence stop: 631.

Location/Qualifiers

1..631

/organism="Vitis vinifera"

/mol\_type="mRNA"

/db\_xref="taxon:29760"

/clone="VVB104H08"

/tissue\_type="leaf"

/dev\_stage="juvenile and adult"

/clone\_lib="An expressed sequence tag database for abiotic

stressed leaves of Vitis vinifera var. Chardonnay"

/notes="Vector: Lambda Uni-Zap XR, Bluescript SK-; Site 1:

EcoRI; Site 2: XhoI; Library construction was performed

according to Stratagene's recommended protocol for the

Lambda UniZapXR vector and cDNA synthesis kit."

ORIGIN

Alignment Scores:

Pred. No.: 9.18e-10 Length: 631

Score: 205.00 Matches: 54

Percent Similarity: 46.3% Conservative: 21

Best Local Similarity: 33.3% Mismatches: 53

Query Match: 19.6% Indels: 34

DB: 6 Gaps: 5

US-10-723-947-77 (1-187) x CD010195 (1-631)

QY 44 HisHisHisHisHisHisGlySerAlaAlaAasp-----Tyr 55

DB 121 CACCATCATCACCACCACTGCGGTGGAATGATGTTCCGGTTCAGGCAAGAT 180

QY 56 ProValProPro-----ProProAspAsn-----PheAspHisArgArg 68

Db 181 CCTCACTCCGCTCAGAACACCCTGCTGACAATGTTTGAAGTGGATTTCTCTCGA 240  
 Qy 69 ThrTTPThrArgProPheHisGluThrAlaAlaGlyAsnSerSerArgLeuThrLeu 88  
 Db 241 TCAAGCTCTCTGCTTACACTATACAGCTCATCTCTAAGCCAAAGCATTTCTCTTCA 300  
 Qy 89 GluValGlyAla-----GlyGlyGlnHisMetAlaHisLeuValGlnProProAla 105  
 Db 301 GATGTTGGGGTGTCCAGATGGAACTGCAACTCCATGCTCATACATCTCTGCTGCTG 360  
 Qy 106 ArgAlaHisIleValProPheTyrGlyGlyAlaPheThrAsnThrIleSerAsnGluAla 125  
 Db 361 ATGAACAAGTACGCGAGCGCGCGGTCTACTGGAGTCAAGCGACCCCAATTA 420  
 Qy 126 IleMetThrIleAspThrGluMetMetValGlyProAlaHisTyrProThrMetGlnGlu 145  
 Db 421 -----TCTGGAATGGAT 432  
 Qy 146 ArgAlaAlaLysValMetArgTyrArgGlyLysArgGlyAsnSerSerArgLeuThrLeu 165  
 Db 433 CGCGAAGCGAGGTGTGAGGTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 492  
 Qy 166 IleArgTyrGluSerArgLysAlaTyrAlaGluLeuArgProArgValAsnGlyArgPhe 185  
 Db 493 ATCAGATACGCTCCAGAAAGCTACGCGAGACGCGTCCAAAGAAATCAGAGCGCGTTTC 552  
 Qy 186 Vallys 187  
 Db 553 GCAAG 558  
 RESULT 13  
 CD010575  
 LOCUS  
 DEFINITION  
 CD010575 650 bp mRNA linear EST 02-MAY-2003  
 VVB113D03 342669 An expressed sequence tag database for abiotic  
 stressed leaves of Vitis vinifera var. Chardonnay Vitis vinifera  
 cDNA clone VVB113D03 5, mRNA sequence.  
 CD010575  
 CD010575.1 GI:30327313  
 EST.  
 SOURCE  
 Vitis vinifera  
 Vitis vinifera  
 ORGANISM  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
 rosids; Vitaceae; Vitis.  
 1 (bases 1 to 650)  
 Cramer,G.R. and Cushman,J.C.  
 An expressed sequence tag database for abiotic stressed leaves of  
 Vitis vinifera var. Chardonnay  
 Unpublished (2002)  
 Contact: Cushman JC  
 Department of Biochemistry  
 University of Nevada  
 MS200, Reno, NV 89557-0014, USA  
 Tel: 775-784-1918  
 Fax: 775-784-1650  
 Email: jcushman@unr.edu  
 PCR Primers  
 FORWARD: T3 20mer  
 BACKWARD: T7 21mer (backward)  
 Plate: 1 row: D column: 03  
 Seq primer: T3 20mer  
 High quality sequence stop: 650.  
 Location/Qualifiers  
 1. 650  
 /organism="Vitis vinifera"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:29760"  
 /clone="VVB113D03"  
 /tissue\_type="leaf"  
 /dev\_stage="juvenile and adult"  
 /clone\_lib="An expressed sequence tag database for abiotic  
 stressed leaves of Vitis vinifera var. Chardonnay"  
 /note="Vector: Lambda Uni-Zap XR, Bluescript SK-; Site\_1:

BcoRI; Site 2: XhoI; Library construction was performed  
 according to Stratagene's recommended protocol for the  
 Lambda UnizapXR vector and cDNA synthesis kit."

## ORIGIN

Alignment Scores:  
 Pred. No.: 9,548-10 Length: 650  
 Score: 205.00 Matches: 54  
 Percent Similarity: 46.3% Conservative: 21  
 Best Local Similarity: 33.3% Mismatches: 53  
 Query Match: 19.6% Indels: 34  
 DB: 6 Gaps: 5

US-10-723-947-77 (1-187) x CD010575 (1-650)

Qy 44 HisHisHisHisHisHisGlySerAlaAlaAap-----Tyr 55  
 Db 121 CACCATCATCACCACCTGCGGTGGAATGATGTAGTTCGCGTTCAAGCCAAAGAT 180  
 Qy 56 ProValProPro-----ProProAspAsn-----PheAspHisArgArg 68  
 Db 181 CCTCACCTCCGCTCAGCAACCCACCTGCTGACAATGTTTGAAGTGGATTTCTCTCGA 240  
 Qy 69 ThrTTPThrArgProPheHisGluThrAlaAlaGlyAsnSerSerArgLeuThrLeu 88  
 Db 241 TCAAGCTCTCTGCTCACAACCTATACAGCTCAATCTCTAAGCCAAAGCATTTCTCTTCA 300  
 Qy 89 GluValGlyAla-----GlyGlyGlnHisMetAlaHisLeuValGlnProProAla 105  
 Db 301 GATGTTGGGGTGTCCAGATGGAACTGCAACTGCTGATCATCTCTACCTTACCTCTCG 360  
 Qy 106 ArgAlaHisIleValProPheTyrGlyGlyAlaPheThrAsnThrIleSerAsnGluAla 125  
 Db 361 ATGAACAAGTACGCGAGCGCGCGGTCTACTGGAGTCAAGCGACCCCAATTA 420  
 Qy 126 IleMetThrIleAspThrGluMetMetValGlyProAlaHisTyrProThrMetGlnGlu 145  
 Db 421 -----TCTGGAATGGAT 432  
 Qy 146 ArgAlaAlaLysValMetArgTyrArgGlyLysArgLysArgTyrAspLysGln 165  
 Db 433 CGCGAAGCGAGGTGTGAGGTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 492  
 Qy 166 IleArgTyrGluSerArgLysAlaTyrAlaGluLeuArgProArgValAsnGlyArgPhe 185  
 Db 493 ATCAGATACGCTCCAGAAAGCTACGCGAGACGCGTCCAAAGAAATCAGAGCGCGTTTC 552  
 Qy 186 Vallys 187  
 Db 553 GCAAG 558

## RESULT 14

## LOCUS

## DEFINITION

BM436387 712 bp mRNA linear EST 31-JAN-2002  
 VVA003D01 52357 An expressed sequence tag database for abiotic  
 stressed leaves of Vitis vinifera var. Chardonnay Vitis vinifera  
 cDNA clone VVA003D01 5, mRNA sequence.

## ACCESSION

## VERSION

## KEYWORDS

## SOURCE

## ORGANISM

BM436387  
 BM436387.1 GI:18458109  
 EST.  
 Vitis vinifera  
 Vitis vinifera

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## COMMENT

## JOURNAL

## COMMENT

## JOURNAL

## COMMENT

## JOURNAL

## COMMENT

## JOURNAL

## COMMENT

MS200, Reno, NV 89557-0014, USA  
Tel: 775-784-1918  
Fax: 775-784-1650  
Email: jcsushman@unr.edu

## PCR Primers

FORWARD: T3 20mer

BACKWARD: T7 21mer

Plate: 003 row: D column: 01

Seq primer: T3 20mer

High quality sequence stop: 712.

## FEATURES

Location/Qualifiers  
1..712  
/organism="Vitis vinifera"  
/mol\_type="mRNA"  
/db\_xref="taxon:29760"  
/clone="VVA003D01"  
/tissue\_type="leaf"  
/dev\_stage="juvenile and adult"  
/clone\_lib="An expressed sequence tag database for abiotic stressed leaves of Vitis vinifera var. Chardonnay"  
/notes="Vector: Lambda Uni-Zap XR, Bluescript SK-, Site 1: EcoRI; Site 2: XhoI; Library construction was performed according to Stratagene's recommended protocol for the Lambda UniZapXR vector and cDNA synthesis kit."

## ORIGIN

Alignment Scores:  
Pred. No.: 1,07e-09 Length: 712  
Score: 205.00 Matches: 54  
Percent Similarity: 46.3% Conservative: 21  
Best Local Similarity: 33.3% Mismatches: 53  
Query Match: 19.6% Indels: 34  
DB: 3 Gaps: 5

US-10-723-947-77 (1-187) x BM436387 (1-712)

Qy 44 HisHisHisHisHisHisGlySerAlaAlaAAsp-----Tyr 55  
Db 232 CACCATCATCACCACCACTCGCGGTGGAATGTTGTTAGTTCGCGTTCAAGCCAAAGAT 291  
Qy 56 ProValProPro-----ProProAspAsn-----PheAspHisArgArg 68  
Db 292 CCTCATCTCCGTCTACGAACCAACCCTGCTGACAAATGTTTGAACCTGGATTTCTCTCGA 351  
Qy 69 ThrTrpThrArgProPheHisGluThrAlaAlaAlaGlyAsnSerSerArgLeuThrleu 88  
Db 352 TCAAAGCTCTCGCTTACAACTATACAGCTCAATCTCTAAGCCAAAGCAATTTTCATCTTCA 411  
Qy 89 GluValGlyAla-----GlyGlyGlnHisMetAlaHisLeuValGlnProProAla 105  
Db 412 GATGTTGGGGTGTCCCATGGAAGTCACTCCATCTGTGTATACATCTCTACCTTCG 471  
Qy 106 ArgAlaHisIleValProPheTyrGlyGlyAlaPheThrAsnThrIleSerAsnGluAla 125  
Db 472 ATGAACAAGTGAGCGAGCGCGCGGGTCTTACTGGAGTCAAGCCGCAATTA 531  
Qy 126 IleMetThrIleAspThrGluMetMetValGlyProAlaHisTyrProThrMetGlnGlu 145  
Db 532 -----TCTGGAATGGAT 543  
Qy 146 ArgAlaAlaLysValMetArgTyrArgGluLysArgArgArgTyrAspLysGln 165  
Db 544 CCGAAGCCAGGTGTGTAGGTACAGAGAGAGAGAGAAACCGGAATTCAGAAAC 603  
Qy 166 IleArgTyrGluSerArgLysAlaTyrAlaGluLeuArgProArgValAsnGlyArgPhe 185  
Db 604 ATCAGATACGCTCCAGAAAGGCTACCGCGAGACCGCTCAAGATCAAGCGCGCTTC 663  
Qy 186 ValLys 187  
Db 664 GCAAAG 669  
RESULT 15

## CZ787328/c

## LOCUS

## DEFINITION

## ACCESSION

## VERSION

## KEYWORDS

## SOURCE

## ORGANISM

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## COMMENT

## FEATURES

## source

## Location/Qualifiers

## 1..546

## /organism="Oryza coarctata"

## /mol\_type="genomic DNA"

## /db\_xref="taxon:77588"

## /clone="OC\_Ba0151B03"

## /tissue\_type="leaves"

## /dev\_stage="mature"

## /lab\_host="DH10B"

## /clone\_lib="OC\_Ba"

## /note="Vector: pAGIBAC1; Site\_1: HindIII; Site\_2: HindIII"

## ORIGIN

## Alignment Scores:

## Pred. No.:

## Score:

## Percent Similarity:

## Best Local Similarity:

## Query Match:

## DB:

## Length:

## Matches:

## Conservative:

## Mismatches:

## Indels:

## Gaps:

## US-10-723-947-77 (1-187) x CZ787328 (1-546)

## Qy 91 GlyAlaGlyGlyGlnHisMetAlaHisLeuValGlnProProAlaArgAlaHisIle-Va 110

## Db 392 GGGGCGAGCGCG-----GTCCGGTCCCACTTCAT 363

## Qy 110 lProPheTyrGlyGlyAlaPheThrAsnThrIleSerAsnGluAlaIleMetThrIleAs 130

## Db 362 GCCATTCTCGGGAGCACACTTGAAGGCACCTTG---AACGATAGCAACAGAGAGGTTGG 306

## Qy 130 pThrGluMetMetValGlyProAlaHisTyrProThrMetGlnGluArgAlaAlaLysVa 150

## Db 305 GGAAGGCATGACGGCGCGCGCGAGT-----GACCTGGCAATCGAGAGGAGGAGCCAAAG 252

## Qy 150 lMetArgTyrArgGluLysArgLysArgArgTyrAspLysGlnIleArgTyrGluSe 170

## Db 251 CATGAGGTACAAAGAGAGAGAGAGAGAGAGAGGAGGTACAGAGAGAGATACGATATGCCTC 192

## Qy 170 rArgLysAlaTyrAlaGluLeuArgProArgValAsnGlyArgPheValLys 187

## Db 191 GAGGAAGGCTATCTCTGAGATGAGGCAAGGTTAAAGGGCGGTTTCGCAAG 140

CZ787328 546 bp DNA linear GSS 26-JUL-2005  
OC\_Ba0151B03.f OC\_Ba Oryza coarctata genomic clone OC\_Ba0151B03  
5', genomic survey sequence.

CZ787328

CZ787328.1 GI:71227181

GSS.

Oryza coarctata (Porteresia coarctata)

Oryza coarctata

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 546)

Kim H., Collura, K., Wissotski, M., Byrne, M., Stum, D., Smart, D.,

Rao, X., Luo, M., Jetty, R., Kudrna, D., Muller, C., Soderlund, C. and

Wing, R.

OMAP (Oryza Map Alignment Project)- Arizona Genomics Institute

Unpublished (2005)

Contact: Rod A. Wing

Arizona Genomics Institute

University of Arizona

Forbes Building Room 303, Tucson, AZ 85721-0036, USA

Tel: 520 626 9595

Fax: 520 621 1259

Email: rwing@genome.arizona.edu

PCR Primers

FORWARD: TAA TAC GAC TCA CTA TAG GG

BACKWARD: CAC TCA TTA GGC ACC CCA

Plate: 0151 row: B column: 03

Seq primer: TAA TAC GAC TCA CTA TAG GG

Class: BAC ends.

Location/Qualifiers

1..546

/organism="Oryza coarctata"

/mol\_type="genomic DNA"

/db\_xref="taxon:77588"

/clone="OC\_Ba0151B03"

/tissue\_type="leaves"

/dev\_stage="mature"

/lab\_host="DH10B"

/clone\_lib="OC\_Ba"

/note="Vector: pAGIBAC1; Site\_1: HindIII; Site\_2: HindIII"

Search completed: February 23, 2006, 11:40:49  
Job time : 3670 secs

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GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: February 23, 2006, 10:37:57 ; Search time 490 Seconds

(without alignments)  
2543.464 Million cell updates/sec

Title: US-10-723-947-77

Perfect score: 1048

Sequence: 1 MSMSGCLGANNCPRLWSP.....YESRKAYAEIPLRVNGRFVK 187

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 4986997 seqs, 332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+pn.model -DEV=xl  
-Q=/abs/ABSWEB\_spool/US10723947/runat\_23022006\_085355\_16167/app\_query.fasta.1  
-DB=N Geneseq -QFMT=fastap -SUFFIX=p2n.rng -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000 -HOST=abs03p  
-USER=US10723947 @CGN\_1\_1\_1096 @runat\_23022006\_085355\_16167 -NCPU=6 -ICPU=3  
-NO MMAP -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120  
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7  
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

N Geneseq 21.\*

1: Geneseqn1980s.\*  
2: Geneseqn1990s.\*  
3: Geneseqn2000s.\*  
4: Geneseqn2001as.\*  
5: Geneseqn2001bs.\*  
6: Geneseqn2002as.\*  
7: Geneseqn2002bs.\*  
8: Geneseqn2003as.\*  
9: Geneseqn2003bs.\*  
10: Geneseqn2003cs.\*  
11: Geneseqn2003ds.\*  
12: Geneseqn2004as.\*  
13: Geneseqn2004bs.\*  
14: Geneseqn2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result	No.	Score	Match	Length	ID	Description
1	1035	98.8	996	13	ADS19577	ADS19577 One grain
2	907.5	86.6	975	13	ADS19581	ADS19581 Langdon (
3	816	77.9	7051	13	ADS19576	ADS19576 One grain
4	768.5	73.3	639	13	ADS19590	ADS19590 Winter ba

5	756	72.1	642	13	ADS19593	ADS19593 Winter ba
6	730.5	69.7	639	13	ADS19584	ADS19584 One grain
7	729.5	69.6	639	13	ADS19587	ADS19587 Langdon (
8	670.5	64.0	2913	13	ADS19580	ADS19580 Langdon (
9	590	56.3	1985	13	ADS19589	ADS19589 Winter ba
10	572.5	54.6	2043	13	ADS19592	ADS19592 Winter ba
11	547.5	52.2	5734	13	ADS19583	ADS19583 One grain
12	538	51.3	3454	13	ADS19586	ADS19586 Langdon (
13	258	24.6	1078	13	ADS16783	ADS16783 Lhd4-rela
14	255	24.3	1078	13	ADS16786	ADS16786 Lhd4-rela
15	254	24.2	1078	13	ADS16780	ADS16780 Lhd4-rela
16	207	19.8	1068	12	ADN72948	ADN72948 Thale cre
17	207	19.8	1297	6	ABN98249	ABN98249 Arabidops
18	207	19.8	1370	13	ADX31777	ADX31777 Plant ful
19	207	19.8	1374	3	AAC46126	AAC46126 Arabidops
20	207	19.8	1377	3	AAC32926	AAC32926 Arabidops
21	207	19.8	1404	13	ADX30238	ADX30238 Plant ful
22	199.5	19.0	1703	14	ADM16416	ADM16416 E Grandis
23	198.5	18.9	1122	13	ADV09279	ADV09279 B. pendul
24	194	18.5	1388	14	AE865256	AE865256 Rice geno
25	193.5	18.5	1728	14	ADM16414	ADM16414 E Grandis
26	189.5	18.1	1385	13	ADX51649	ADX51649 Plant ful
27	188.5	18.0	2723	13	ADS16785	ADS16785 Lhd4-rela
28	188.5	18.0	2723	13	ADS16782	ADS16782 Lhd4-rela
29	188	17.9	1101	2	AAT29510	AAT29510 CONSTANS
30	187.5	17.9	2723	13	ADS16779	ADS16779 Lhd4-rela
31	185.5	17.7	577	12	ADJ39390	ADJ39390 Plant cDN
32	184.5	17.6	1441	13	ADT20147	ADT20147 Plant cDN
33	183	17.5	1406	14	ADM16807	ADM16807 Pinus rad
34	180.5	17.2	1101	2	AAT29509	AAT29509 CONSTANS
35	180	17.2	698	13	ADX31789	ADX31789 Plant ful
36	180	17.2	971	3	AAC51945	AAC51945 Arabidops
37	180	17.2	1125	3	AAC46448	AAC46448 Arabidops
38	180	17.2	1202	13	ADX45392	ADX45392 Plant ful
39	180	17.2	1553	13	ADX13438	ADX13438 Plant ful
40	180	17.2	1593	13	ADT14899	ADT14899 Plant cDN
41	179	17.1	939	4	AAC90637	AAC90637 Strawberry
42	176.5	16.8	596	13	ACN60093	ACN60093 Cotton gy
43	176.5	16.8	885	6	ABZ12460	ABZ12460 Arabidops
44	176.5	16.8	1002	12	ADJ39403	ADJ39403 Plant cDN
45	176.5	16.8	1075	13	ADX47666	ADX47666 Plant ful

## ALIGNMENTS

RESULT 1  
ADS19577  
ID ADS19577 standard; cDNA; 996 BP.  
AC ADS19577;  
XX ADS19577;  
DT 30-DEC-2004 (first entry)  
DE One grained wheat DV92 ZCCT1 cDNA.  
XX One grained wheat; chromosome 5a; ss; APTALAL; API; vernalisation;  
KW One grained wheat; chromosome 5a; ss; APTALAL; API; vernalisation;  
KW flowering; ZCCT1; ZCCT2; vrn1; vrn2; CARG box; plant; gene.  
XX Triticum monococcum.  
XX US2004205848-A1.  
XX 14-OCT-2004.  
XX 26-NOV-2003; 2003US-00723947.  
XX 11-APR-2003; 2003US-00412137.  
XX (REGC ) UNIV CALIFORNIA.  
XX Dubcovsky J, Yan L, Loukoianov A;  
XX WPI, 2004-728059/71.



DR P-PSDB; ADS19578.  
XX. New recombinant ZCCT1 protein coding sequence useful for altering a  
PT plant's (e.g., wheat, barley, rye, oats, or forage grasses) response to  
PT vernalization or flowering times.  
XX  
XX  
PS Claim 1; SEQ ID NO 75; 115pp; English.  
XX  
XX The invention relates to a recombinant ZCCT1 protein (2n finger and CCT  
CC domain protein) coding sequence comprising a nucleic acid that hybridizes  
CC to the barley ZCCT1 cDNA appearing as ADS19577. The patent also discloses  
CC the identification of to genes, vrn1 identified as APL (APETALA1) and  
CC vrn2 identified as ZCCT1 controlling vernalisation of flowering in  
CC temperate grasses. ZCCT1 also has a duplicate gene ZCCT2, all three genes  
CC have been localised to chromosome 5a of one grained wheat, Triticum  
CC monococcum. ZCCT1 is the repressor of APL whose promoter contains a  
CC binding site for ZCCT1 termed the CARG box. Also included are a vector  
CC comprising the recombinant ZCCT1 protein coding sequence above, a cell  
CC comprising the vector, a transgenic plant comprising the recombinant  
CC ZCCT1 protein coding sequence above (or a genetic construct that inhibits  
CC ZCCT1 repression of APL), a seed from the transgenic plant, a method for  
CC altering a plant's response to vernalisation and a molecular marker for  
CC vrn2 derived from ADS19577. The genetic construct is an interference RNA  
CC construct (RNAi) that inhibits ZCCT1 activity and comprises an antisense  
CC construct that inhibits ZCCT1 activity, a nucleic acid sequence encoding  
CC a repression defective ZCCT1 protein operably linked to a promoter or a  
CC nucleic acid sequence encoding a DNA binding defective ZCCT1 protein  
CC operably linked to a promoter. The present sequence is a plant ZCCT1 cDNA  
CC sequence.  
XX  
SQ Sequence 996 BP; 281 A; 273 C; 224 G; 218 T; 0 U; 0 Other;  
  
Alignment Scores:  
Pred. No.: 7,23e-86 Length: 996  
Score: 1035.00 Matches: 185  
Percent Similarity: 99.5% Conservativity: 1  
Best Local Similarity: 98.9% Mismatches: 1  
Query Match: 98.8% Indels: 0  
DB: 13 Gaps: 0  
  
US-10-723-947-77 (1-187) x ADS19577 (1-996)  
  
QY 1 MetSerMetSerCysGlyLeuCysGlyAlaAsnAsnCysProArgLeuMetValSerPro 20  
DB 109 ATGTCATATCATCGGTTTGTGCGCGCCCAACACTGCCGCGCTCATGCTCTCGCC 168  
  
QY 21 IleHisHisHisHisHisGlnGlnHisGlnLeuCysGlyTyrGlnPhePheAla 40  
DB 169 ATTACCATCATCATCACCATCATCATGAGGACACAGCTGTGTGAGTACAGTTCTTCGCC 228  
  
QY 41 HisGlyAsnHisHisHisHisHisHisGlySerAlaAlaAspTyrProValProProPro 60  
DB 229 CATGCAACACCACCACCACCACCACCATGCTCGGAGCAGAGATCCAGTGCACCGCG 288  
  
QY 61 ProAspAsnPhaAspHisArgThrTrpThrArgProPheHisGluThrAlaAlaAla 80  
DB 289 CCAGACAACTTCGACCACCGAGAACATGGACAGACACCATTTTCATGAACAGCAGCGCA 348  
  
QY 81 GlyAsnSerSerArgLeuThrLeuGluValGlyAlaGlyGlyHisMetAlaHisLeu 100  
DB 349 GGGAAACAGCAGAGGCTTCAGCTGGAGGTGGCGGAGCGGCGCAACACATGGCTCACCTA 408  
  
QY 101 ValGlnProProAlaArgAlaHisIleValProPheTyrGlyGlyAlaPheThrAsnThr 120  
DB 409 GTGCGACCAACCGGACAGACCCACATCGTGCATTTACGGAGGTGCATTCACCAACT 468  
  
QY 121 IleSerAsnGluAlaIleMetThrIleAspThrGluMetMetValGlyProAlaHisTyr 140  
DB 469 ATTAGCAATGAGCAATCATGACTATTTCACAGAGATGATGTTGGGGCTGCCCATATT 528  
  
QY 141 ProThrMetGlnGluArgAlaAlaValMetArgTyrArgGluHisArgLysArgArg 160  
DB 529 CCCACAATCAGGAGAGACGAGGAGGATGATGAGGTATAGGAGAGAGGAGGAGCGG 588

QY 161 ArgTyrAspLysGlnIleArgTyrGluSerArgLysAlaTyrAlaGluLeuArgProArg 180  
DB 599 CGCTATGACAAAGCAATCCGATACGAGTCCAGAAAGCTTACGCTGAGCTTCGGCCATGG 648  
  
QY 181 ValaGngLyArgPheValLys 187  
DB 649 GTCAACGGCGCTTTGTCAAG 669

RESULT 2  
ADS19581  
ID ADS19581 standard; cDNA; 975 BP.  
XX  
AC ADS19581;  
XX  
DT 30-DEC-2004 (first entry)  
XX  
DE Langdon (tetraploid) wheat ZCCT1 cDNA.  
XX  
KW Wild emmer wheat; ss; APETALA1; APL; vernalisation; flowering; ZCCT1;  
XX ZCCT2; vrn1; vrn2; CARG box; plant; gene.  
XX  
OS Triticum turgidum; subsp. dicoccoides.  
XX  
PN US2004205848-A1.  
XX  
PD 14-OCT-2004.  
XX  
PF 26-NOV-2003; 2003US-00723947.  
XX  
PR 11-APR-2003; 2003US-00412137.  
XX  
PA (REGC) UNIV CALIFORNIA.  
XX  
PI Dubcovsky J, Yan L, Loukoianov A;  
XX  
DR WPI; 2004-728059/71.  
DR P-PSDB; ADS19582.  
XX  
PT New recombinant ZCCT1 protein coding sequence useful for altering a  
PT plant's (e.g., wheat, barley, rye, oats, or forage grasses) response to  
PT vernalization or flowering times.  
XX  
PS Disclosure; SEQ ID NO 79; 115pp; English.  
XX  
CC The invention relates to a recombinant ZCCT1 protein (2n finger and CCT  
CC domain protein) coding sequence comprising a nucleic acid that hybridizes  
CC to the barley ZCCT1 cDNA appearing as ADS19577. The patent also discloses  
CC the identification of to genes, vrn1 identified as APL (APETALA1) and  
CC vrn2 identified as ZCCT1 controlling vernalisation of flowering in  
CC temperate grasses. ZCCT1 also has a duplicate gene ZCCT2, all three genes  
CC have been localised to chromosome 5a of one grained wheat, Triticum  
CC monococcum. ZCCT1 is the repressor of APL whose promoter contains a  
CC binding site for ZCCT1 termed the CARG box. Also included are a vector  
CC comprising the recombinant ZCCT1 protein coding sequence above, a cell  
CC comprising the vector, a transgenic plant comprising the recombinant  
CC ZCCT1 protein coding sequence above (or a genetic construct that inhibits  
CC ZCCT1 repression of APL), a seed from the transgenic plant, a method for  
CC altering a plant's response to vernalisation and a molecular marker for  
CC vrn2 derived from ADS19577. The genetic construct is an interference RNA  
CC construct (RNAi) that inhibits ZCCT1 activity and comprises an antisense  
CC construct that inhibits ZCCT1 activity, a nucleic acid sequence encoding  
CC a repression defective ZCCT1 protein operably linked to a promoter or a  
CC nucleic acid sequence encoding a DNA binding defective ZCCT1 protein  
CC operably linked to a promoter. The present sequence is a plant ZCCT1 cDNA  
CC sequence.  
XX  
SQ Sequence 975 BP; 276 A; 263 C; 218 G; 218 T; 0 U; 0 Other;

Alignment Scores:  
Pred. No.: 3.91e-74 Length: 975  
Score: 907.50 Matches: 168  
Percent Similarity: 91.4% Conservativity: 3



Db 3421 TGAATACACCCACTACAAAAAGTAGCACCATGTAACCAATTCATATATTTCTTCACATAA 3480  
QY 109 ----- 109  
Db 3481 TTCGTGTAATTTAGCGTCTCGATGTTCTCCTGAAAAAGATATACGGGAATGGATCTGG 3540  
QY 109 ----- 109  
Db 3541 ATATCTCTTAATTTCTATGGAGGCATAGAGTTGTGTTTGTATTAGTTAGTCAGAAAT 3600  
QY 109 ----- 109  
Db 3601 TGTATGGGTTGTCAATCATCATCTCATATATATCTTATTTCTTTTGTGACCAAC 3660  
QY 109 ----- 109  
Db 3661 AGAAGGTAATCAGTCATACATGCATCTGAAAATTAGACTTGTGTGCAATACTAATA 3720  
QY 109 ----- 109  
Db 3721 ACCAACTCGACGGCACAGCTGGGGGAAGACTTTAATCAAGCTGTAGCTAGAGCTTAAT 3780  
QY 109 ----- 109  
Db 3781 AATATAACATATCTTTATGGATCAAGCAATACATATACGCTCAATTTCTCAACTTGT 3840  
QY 109 ----- 109  
Db 3841 AATATCTATCTGGAGTCCACACTTTATGTAATTAATGACAAAGTTTGTGNAATGGAC 3900  
QY 109 ----- 109  
Db 3901 AATATACATAGTGGATCGATGCACCCTTTTCTCAATTTATGTTGCTCAATTAATGATT 3960  
QY 109 ----- 109  
Db 3961 GTTATTTAGTATTTCAATTTATCTTGAGCTAGTATTTTGGCAAGTCTGTAGCTCATATATA 4020  
QY 109 ----- 109  
Db 4021 CTGATACTACTCCACGATAGCTTGGTAGTGGCGGGTGATCGATCTACCGAGTTTAT 4080  
QY 109 ----- 109  
Db 4081 AAAAAGTATGATCGATCGGTCCAAAAAGAACAAACCCATACAAAAATGGAAGAGATCC 4140  
QY 109 ----- 109  
Db 4141 TTGTTTAGTTAGTTTGTGATCAGAAAAATGCGCTAATTTAGTTAGTCTGTCTATCAATCTTTTGA 4200  
QY 109 ----- 109  
Db 4201 ACATGCGATGTTTACCCCAACCGACCCAGATCAATTTATGATGAAGTTAGCGCTTTT 4260  
QY 109 ----- 109  
Db 4261 AAAAAGTATGATGATCATATCATATGATCAGGGCTACACATGTACATATAACCTTA 4320  
QY 109 ----- 109  
Db 4321 ATTAAAAAGTATATTTGTAGACCAATTTGATTTTGGACGGTGGCATCTTTTGGAAAAAAA 4380  
QY 109 ----- 109  
Db 4381 TGGCAGAGGATGTTAGTCTTCCATGTCAGAAATAGATGTTACATCAATCAAGTGCATC 4440  
QY 109 ----- 109  
Db 4441 TCTGAATGAATGGATCATTTTCTAGTTAATTAGAGACCAATTAGATCTTCTATAACA 4500  
QY 109 ----- 109  
Db 4501 GGGGAGTATCAAGTACGTATCTGCTACCCATAAGAAAGTACATACTGCGATCTTATGAT 4560

QY 110 -----ValProPheTyrGlyValaPheThrAsnThrIleSer 122  
Db 4561 TATTTTCTCTTGTGATGTTCCAGGTGCCATTTACGAGGAGTGATTCACCAACTATTAGC 4620  
QY 123 AenGluAlaIleMetThrIleAspThrGluMetMetValGlyProAlaHisTyrProThr 142  
Db 4621 AATGAAGCAATCATGACTATTGCACAGAGATGATGGTGGGCGCTGCCCATTTATCCACA 4680  
QY 143 MetGlnGluAtgAlaAlaLysValMetArgTyrArgGluLysArgLysArgArgArgTyr 162  
Db 4681 ATCCAGGAGAGACAGCAGAGGTGATGAGGTATAGGAGAGAGAGAGAGGCGGCTAT 4740  
QY 163 AspLysGlnIleArgTyrGluSerArgLysAlaTyrAlaGluLeuArgProArgValAsn 182  
Db 4741 GACAAAGCAATCCGATACGATCCAGAAAGCTTACGCTGAGCTTCGGCCATGGGTCAAC 4800  
QY 183 GlyArgPheValLys 187  
Db 4801 GGCCGCTTTGTCAAG 4815

## RESULT 4

ADSI9590  
ID ADSI9590 standard; cDNA; 639 BP.

AC  
ADSI9590;

DT 30-DEC-2004 (first entry)

XX Winter barley ZCCT-Ha cDNA.

DE Barley; ss; APETALAI; API; vernalisation; flowering; ZCCT1; ZCCT2; vrnl1;

KW vrnl2; CarG box; plant; gene.

XX Hordeum vulgare.

XX US2004205848-A1.

PN 14-OCT-2004.

PD 26-NOV-2003; 2003US-00723947.

PF 11-APR-2003; 2003US-00412137.

PR (REGC) UNIV CALIFORNIA.

XX Dubcovsky J, Yan L, Loukoianov A;

XX WPI; 2004-728059/71.

DR P-PSDB; ADSI9591.

PT New recombinant ZCCT1 protein coding sequence useful for altering a  
PT plant's (e.g., wheat, barley, rye, oats, or forage grasses) response to  
PT vernalization or flowering times.

PS Disclosure; SEQ ID NO 88; 115bp; English.

XX The invention relates to a recombinant ZCCT1 protein (Zn finger and CCT  
XX domain protein) coding sequence comprising a nucleic acid that hybridizes  
XX to the barley ZCCT1 cDNA appearing as ADSI9577. The patent also discloses  
XX the identification of to genes, vrnl identified as API (APETALAI) and  
XX vrnl2 identified as ZCCT1 controlling vernalisation of flowering in  
XX temperate grasses. ZCCT1 also has a duplicate gene ZCCT2, all three genes  
XX have been localised to chromosome 5a of one grained wheat, Triticum  
XX monococcum. ZCCT1 is the repressor of API whose promoter contains a  
XX binding site for ZCCT1 termed the CarG box. Also included are a vector  
XX comprising the recombinant ZCCT1 protein coding sequence above, a call  
XX comprising the vector, a transgenic plant comprising the recombinant  
XX ZCCT1 protein coding sequence above (or a genetic construct that inhibits  
XX ZCCT1 repression of API), a seed from the transgenic plant, a method for  
XX altering a plant's response to vernalisation and a molecular marker for  
XX vrnl2 derived from ADSI9577. The genetic construct is an interference RNA  
XX construct (RNAi) that inhibits ZCCT1 activity and comprises an antisense

CC construct that inhibits ZCCT1 activity, a nucleic acid sequence encoding  
CC a repression defective ZCCT1 protein operably linked to a promoter or a  
CC nucleic acid sequence encoding a DNA binding defective ZCCT1 protein  
CC operably linked to a promoter. The present sequence is a plant ZCCT cDNA  
CC sequence.

XX  
SQ Sequence 639 BP; 164 A; 208 C; 159 G; 108 T; 0 U; 0 Other;

Alignment Scores:  
Pred. No.: 1 48e-61 Length: 639  
Score: 768.50 Matches: 148  
Percent Similarity: 82.6% Conservativity: 9  
Best Local Similarity: 77.9% Mismatches: 28  
Query Match: 73.3% Indels: 5  
DB: 13 Gaps: 3

US-10-723-947-77 (1-187) x ADS19590 (1-639)

QY 1 MetSerMetSerCysGlyLeuCysGlyAlaAsnAsnCysProArgLeuMetValSerPro 20  
DB 1 ATGTCCATGTCATGTGGTTGTGCGCGCCAGCAACTGCGCGTACCACATGATGTCGCC 60  
QY 21 IleHisHisHisHisHisHisHisHisHisHisHisHisHisHisHisHisHisHisHis 40  
DB 61 GTTCTTCTTCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 120  
QY 41 HisGlyAsnHisHisHisHisHisHisHisHisHisHisHisHisHisHisHisHisHis 59  
DB 121 CAAGGT-----CACCACCAACCAACCAACCAACCAACCAACCAACCAACCAACCA 174  
QY 60 ProProAspAsnPheAspHisArgArgThrTrpThrArgProPheHisGluThrAlaAla 79  
DB 175 CGCCAGACAAATGCCACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCA 234  
QY 80 AlaGlyAsnSerSerArgLeuThrLeuGluValGlyAlaGlyGlyGlnHisMetAlaHis 99  
DB 235 CCAGAGAACAGACACAGGCTCACACGGGAGGTGGACGGCGGCGGCGGCGGCGGCGGCTAC 294  
QY 100 LeuValGlnProProAla-----ArgAlaHisIleValProPheThrGlyGlyAlaPhe 117  
DB 295 CTGCTCGACCCACCGCT 354  
QY 118 ThrAsnThrIleSerAsnGluAlaIleMetThrIleAspThrGluMetMetValGlyPro 137  
DB 355 GCCAGCACTATTAGCAACGCAACGATCATGACTATTATACAGAAATGATGGGGCTCT 414  
QY 138 AlaHisTyProThrMetGlnGluAlaAlaLysValMetArgTyArgGluLysArg 157  
DB 415 GCCTATAATCCACGATGCAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 474  
QY 158 LysArgArgArgTyArgAspLysGlnIleArgTyGluSerArgLysAlaTyAlaGluLeu 177  
DB 475 AGAGCGCGCGCTTATGACAAAGCAAAATCCGCTACGAGTCCAGAAAGCTTACCGCGGAGCTC 534  
QY 178 ArgProArgValAsnGlyArgPheValLys 187  
DB 535 AGGCCACGGGTCAATGGCGCGCTTGGCAG 564

RESULT 5

ADS19593  
ID ADS19593 standard; cDNA; 642 BP.

XX  
AC ADS19593;  
XX  
XX 30-DEC-2004 (first entry)  
XX  
XX winter barley ZCCT-Hb cDNA.  
XX  
XX Barley; ss; APETAL1; AP1; vernalisation; flowering; ZCCT1; ZCCT2; vrn1;  
XX vrn2; CARG box; plant; gene.  
XX  
OS Hordeum vulgare.

PN US2004205848-A1.  
XX  
PD 14-OCT-2004.  
XX  
PF 26-NOV-2003; 2003US-00723947.  
XX  
PR 11-APR-2003; 2003US-00412137.  
XX (REGC ) UNIV CALIFORNIA.  
XX  
XX Dubcovsky J, Yan L, Loukoianov A;  
PI WPI; 2004-728059/71.  
XX P-PSDB; ADS19594.  
DR  
DR  
PT New recombinant ZCCT1 protein coding sequence useful for altering a  
PT vernalization or flowering times.  
PS Disclosure; SEQ ID NO 91; 115pp; English.  
XX  
XX The invention relates to a recombinant ZCCT1 protein (Zn finger and CCT  
domain protein) coding sequence comprising a nucleic acid that hybridises  
to the barley ZCCT1 cDNA appearing as ADS19577. The patent also discloses  
the identification of to genes, vrn1 identified as AP1 (APETAL1) and  
vrn2 identified as ZCCT1 controlling vernalisation of flowering in  
temperate grasses. ZCCT1 also has a duplicate gene ZCCT2, all three genes  
have been localised to chromosome 5a of one grained wheat, Triticum  
monococcum. ZCCT1 is the repressor of AP1 whose promoter contains a  
binding site for ZCCT1 termed the CARG box. Also included are a vector  
comprising the recombinant ZCCT1 protein coding sequence above, a cell  
comprising the vector, a transgenic plant comprising the recombinant  
ZCCT1 protein coding sequence above (or a genetic construct that inhibits  
ZCCT1 repression of AP1), a seed from the transgenic plant, a method for  
altering a plant's response to vernalisation and a molecular marker for  
vrn2 derived from ADS19577. The genetic construct is an interference RNA  
construct (RNAi) that inhibits ZCCT1 activity and comprises an antisense  
construct that inhibits ZCCT1 activity, a nucleic acid sequence encoding  
a repression defective ZCCT1 protein operably linked to a promoter or a  
nucleic acid sequence encoding a DNA binding defective ZCCT1 protein  
operably linked to a promoter. The present sequence is a plant ZCCT cDNA  
sequence.

SQ Sequence 642 BP; 165 A; 206 C; 163 G; 108 T; 0 U; 0 Other;

Alignment Scores:  
Pred. No.: 2 11e-60 Length: 642  
Score: 756.00 Matches: 146  
Percent Similarity: 82.6% Conservativity: 11  
Best Local Similarity: 76.8% Mismatches: 29  
Query Match: 72.1% Indels: 4  
DB: 13 Gaps: 3

US-10-723-947-77 (1-187) x ADS19593 (1-642)

QY 1 MetSerMetSerCysGlyLeuCysGlyAlaAsnAsnCysProArgLeuMetValSerPro 20  
DB 1 ATGTCCATGTCATGCGTTGTGCGCGCCAGCAACTGCGCGTACCACATGATGTCGCC 60  
QY 21 IleHisHisHisHisHisHisHisHisHisHisHisHisHisHisHisHisHisHisHis 40  
DB 61 GTTCTTCTTCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 120  
QY 41 HisGlyAsnHisHisHisHisHisHisHisHisHisHisHisHisHisHisHisHisHis 59  
DB 121 CAAGGT-----CACCACCAACCAACCAACCAACCAACCAACCAACCAACCAACCA 177  
QY 60 ProProAspAsnPheAspHisArgArgThrTrpThrArgProPheHisGluThrAlaAla 79  
DB 178 CGCGCGCGCAATGGCCACCGCGAGATCATGGCCAGCTGTTTCATGAAACAGAGCT 237  
QY 80 AlaGlyAsnSerSerArgLeuThrLeuGluValGlyAlaGlyGlyGlnHisMetAlaHis 99

Db 238 CCAGTGAATAGACACAGGCTCACAAGAGGTGGAGCGGCGGCGCAACAGATGGCTCAC 297  
Qy 100 LeuValGlnProProLa-----ArgAlaHisIleValProPheTyrGlyAlaPhe 117  
|||:|||||  
Db 298 CTGCTGCACCGCGCGCGCGCAAGAGCCACCATGTCCTCCGCGGAGTGCAATTC 357  
Qy 118 ThrAsnThrIleSerAsnGluAlaIleMetThrIleAspThrGluMetValGlyPro 137  
|||:|||||  
Db 358 ACCAACACTATTAGCAACGCAACGATCATGCTATTATACAGAGATGATGGCGGGACT 417  
Qy 138 AlaHisTyrProThrMetGlnGluArgAlaAlaLysValMetArgTyrArgGluLysArg 157  
|||:|||||  
Db 418 GCTATAGTCCACAGATGACGAGAAAGAGAGAGTATGAGGTACAGGAGAGAGAG 477  
Qy 158 LysArgArgArgTyrAspLysGlnIleArgTyrGluSerArgLysAlaTyrAlaGluLeu 177  
|||:|||||  
Db 478 AAGAGCGCGCTATGACAAAGCAAAATCCGCTACGAGTCCAGAAAGCTTACCGCGGCTT 537  
Qy 178 ArgProArgValAsnGlyArgPheValLys 187  
Db 538 AGGCCACGGGTCAACGGCGCTTTGTCAAG 567

## RESULT 6

ADSI19584  
ID ADS19584 standard; cDNA; 639 BP.

AC ADS19584;  
DT 30-DEC-2004 (first entry)

DE One grained wheat DV92 ZCCT2 cDNA.  
KW One grained wheat; chromosome 5a; ss; APETALAI; AP1; vernalisation;  
flowering; ZCCT1; ZCCT2; vrn1; vrn2; CARG box; plant; gene.

XX Triticum monococcum.

XX US20040205848-A1.

PN 14-OCT-2004.

PP 26-NOV-2003; 2003US-00723947.

PR 11-APR-2003; 2003US-00412137.

XX (REGC ) UNIV CALIFORNIA.

XX Dubcovsky J, Yan L, Loukoianov A;

PI WPI; 2004-728059/71.

DR P-PSDB; ADS19585.

XX New recombinant ZCCT1 protein coding sequence useful for altering a  
PT vernalization or flowering times.  
PT  
XX Disclosure; SEQ ID NO 82; 115pp; English.

XX The invention relates to a recombinant ZCCT1 protein (Zn finger and CCT  
CC domain protein) coding sequence comprising a nucleic acid that hybridises  
CC to the barley ZCCT1 cDNA appearing as ADS19577. The patent also discloses  
CC the identification of to genes, vrn1 identified as AP1 (APETALAI) and  
CC vrn2 identified as ZCCT1 controlling vernalisation of flowering in  
CC temperate grasses. ZCCT1 also has a duplicate gene ZCCT2, all three genes  
CC have been localised to chromosome 5a of one grained wheat, Triticum  
CC monococcum. ZCCT1 is the repressor of AP1 whose promoter contains a  
CC binding site for ZCCT1 termed the CARG box. Also included are a vector  
CC comprising the recombinant ZCCT1 protein coding sequence above, a cell  
CC comprising the vector, a transgenic plant comprising the recombinant  
CC ZCCT1 protein coding sequence above (or a genetic construct that inhibits  
CC ZCCT1 repression of AP1), a seed from the transgenic plant, a method for  
CC altering a plant's response to vernalisation and a molecular marker for  
CC Vrn2 derived from ADS19577. The genetic construct is an interference RNA

CC construct (RNAi) that inhibits ZCCT1 activity and comprises an antisense  
CC construct that inhibits ZCCT1 activity, a nucleic acid sequence encoding  
CC a repression defective ZCCT1 protein operably linked to a promoter or a  
CC nucleic acid sequence encoding a DNA binding defective ZCCT1 protein  
CC operably linked to a promoter. The present sequence is a plant ZCCT cDNA  
CC sequence.

SQ Sequence 639 BP; 162 A; 197 C; 171 G; 109 T; 0 U; 0 Other;

## Alignment Scores:

Pred. No.: 4.69e-58 Length: 639  
Score: 730.50 Matches: 144  
Percent Similarity: 81.8% Conservative: 11  
Best Local Similarity: 75.8% Mismatches: 28  
Query Match: 69.7% Indels: 7  
DB: 13 Gaps: 4

US-10-723-947-77 (1-187) x ADS19584 (1-639)

Qy 1 MetSerMetSerCysGlyLeuCysGlyAlaAlaAsnAsnCysProArgLeuMetValSerPro 20

Db 1 ATGTCCATGTCATGCGGTTTGTGGCGCGCAAGAGACTGCCCGCACCATGATGATCTCGCCC 60

Qy 21 IleHisHisHisHisHisHisHisHisHisHisHisHisHisHisHisHisHisHisHis 40

Db 61 GTT-----CTTCAGCATCAGGAACACACACTGGCTGCGGAGTACAGTTCTTCACC 111

Qy 41 HisGlyAsnHisHisHisHisHisHisHisHisHisHisHisHisHisHisHisHisHisHis 60

Db 112 CAAGGC---CACCACCACCACCACCACCAGCGCGCGGGGAGTACCCACCGCCACCGCCA 168

Qy 61 ProAsp---AsnPheAspHisArgArgThrTrpThrArgProPheHisGluThrAlaAla 79

Db 169 CCGTCGGGCAATTCGCCACCTGCAGATCATGAGCACACACCGTTTTCATGAACACAGCAGCT 228

Qy 80 AlaGlyAsnSerSerArgLeuThrLeuGluValGlyAlaGlyGlyGlnHisMetAlaHis 99

Db 229 GCAGGGAACAGCAGCAGACTCAGCTGGAGGTAGATGAGCGGCGGCAAAACATGCTCAC 288

Qy 100 LeuValGlnProProAlaAlaAlaHis-----IleValProPheTyrGlyAlaPhe 117

Db 289 CTGCTGACGACCCCGGCGCAGCCAGAACACCATCGTGCCATCTCGGGGCTGCATTC 348

Qy 118 ThrAsnThrIleSerAsnGluAlaIleMetThrIleAspThrGluMetMetValGlyPro 137

Db 349 ACCAGCACTATTAGCAATGCAACAAATCATGACTATTGATACAGAGATGATGTTGGGGCT 408

Qy 138 AlaHisTyrProThrMetGlnGluArgAlaAlaLysValMetArgTyrArgGluLysArg 157

Db 409 GCCCAATAATCTGACGATGACGAGAGAGAGGAGGAGGTGATGAGGTACAGGAGAGAGG 468

Qy 158 LysArgArgArgTyrAspLysGlnIleArgTyrGluSerArgLysAlaTyrAlaGluLeu 177

Db 469 AAGAGCGGTGCTATGACAGCAAAATCGCTACGAGTCCAGAAAGCTTACCGCGAGCTC 528

Qy 178 ArgProArgValAsnGlyArgPheValLys 187

Db 529 AGGCCACGGGTCAATGGTCTTGTTCAG 558

RESULT 7

ADSI19587

ID ADS19587 standard; cDNA; 639 BP.

XX

XX ADS19587;

XX 30-DEC-2004 (first entry)

XX Langdon (tetraploid) wheat ZCCT2 cDNA.

XX Wild emmer wheat; ss; APETALAI; AP1; vernalisation; flowering; ZCCT1;

XX ZCCT2; vrn1; vrn2; CARG box; plant; gene.

XX Triticum turgidum; subsp. dicoccoides.

OS

XX US2004205848-A1.  
 PN 14-OCT-2004.  
 PD 26-NOV-2003; 2003US-00723947.  
 PF 11-APR-2003; 2003US-00412137.  
 XX (REGC ) UNIV CALIFORNIA.  
 PA Dubcovsky J, Yan L, Loukoianov A;  
 PI WPI: 2004-728059/71.  
 XX P-PSDB; ADS19588.  
 DR New recombinant ZCCT1 protein coding sequence useful for altering a  
 XX plant's (e.g., wheat, barley, rye, oats, or forage grasses) response to  
 PT vernalization or flowering times.  
 PT Disclosure; SEQ ID NO 85; 115pp; English.  
 PS  
 XX The invention relates to a recombinant ZCCT1 protein (Zn finger and CCT  
 CC domain protein) coding sequence comprising a nucleic acid that hybridises  
 CC to the barley ZCCT1 cDNA appearing as ADS19577. The patent also discloses  
 CC the identification of to genes, vrn1 identified as AP1 (APETALA1) and  
 CC vrn2 identified as ZCCT1 controlling vernalisation of flowering in  
 CC temperate grasses. ZCCT1 also has a duplicate gene ZCCT2, all three genes  
 CC have been localised to chromosome 5a of one grained wheat, Triticum  
 CC monococcum. ZCCT1 is the repressor of AP1 whose promoter contains a  
 CC binding site for ZCCT1 termed the CARG box. Also included are a vector  
 CC comprising the recombinant ZCCT1 protein coding sequence above, a cell  
 CC comprising the vector, a transgenic plant comprising the recombinant  
 CC ZCCT1 protein coding sequence above (or a genetic construct that inhibits  
 CC ZCCT1 repression of AP1), a seed from the transgenic plant, a method for  
 CC altering a plant's response to vernalisation and a molecular marker for  
 CC vrn2 derived from ADS19577. The genetic construct is an interference RNA  
 CC construct (RNAi) that inhibits ZCCT1 activity and comprises an antisense  
 CC construct that inhibits ZCCT1 activity, a nucleic acid sequence encoding  
 CC a repression defective ZCCT1 protein operably linked to a promoter or a  
 CC nucleic acid sequence encoding a DNA binding defective ZCCT1 protein  
 CC operably linked to a promoter. The present sequence is a plant ZCCT1 cDNA  
 CC sequence.  
 XX  
 SQ Sequence 639 BP; 161 A; 200 C; 172 G; 106 T; 0 U; 0 Other;

Alignment Scores:  
 Pred. NO.: 5.8e-58 Length: 639  
 Score: 729.50 Matches: 143  
 Percent Similarity: 81.6% Conservative: 12  
 Best Local Similarity: 75.3% Mismatches: 28  
 Query Match: 69.6% Indels: 7  
 DB: 13 Gaps: 4

US-10-723-947-77 (1-187) x ADS19587 (1-639)

QY 1 MetSerMetSerCysGlyLeuCysGlyAlaAsnAsnCysProArgLeuMetValSerPro 20  
 DB 1 ATGCCCATGTCATCGGTTGTGCGCGCAAGCGACTGCCCGCACCACCATGATCTCGCCC 60  
 QY 21 IIEHSH 40  
 DB 61 GTT-----CTTCAGCATCAGGAACAACACCGGCTCGCGGAGTACCAGTCTTCACC 111  
 QY 41 HSH 60  
 DB 112 CAGGCG--CACACACACACACACACGAGCGCGCGGAGTACCCACCGCCACCGCCA 168  
 QY 61 ProAsp---AsnPhaAspHisArgArgThrTrpThrArgProPheHisGluThrAlaLa 79  
 DB 169 CCGTCAGGCAATGTCACCACTGCATGATGACACACCGGTTTCATGAACAGCAGCT 228  
 QY 80 AlaGlyAsnSerSerArgLeuThrLeuGluValGlyAlaGlyGlyGlnHisMetAlaHis 99

DB 229 GCAGGGACAGCAGCAGGCTCAAGCTGGAGGTAGACGCGCGCCAAACATCGCTCAC 288  
 QY 100 LeuValGlnProAlaArgAlaHis-----IleValProPheTyrfGlyGlyAlaPhe 117  
 DB 289 CTGCTGCAGCCACCGGCGCGCGCAAGAACACCATCGTCCATTCTGCGGGGCTGCATTTC 348  
 QY 118 ThrAsnThrIleSerAsnGluAlaIleMetThrIleAspThrGluMetMetValGlyPro 137  
 DB 349 ACCAGCACTATTAGCAATGCAACGATCATGATATTGATACAGAGATGATGTGGGGGCT 408  
 QY 138 AlaHisTyfProThrMetGlnGluArgAlaIleValMetArgTyfArgGluLysArg 157  
 DB 409 GCCCAATAATCTGACGATGCGAGGAGAGAGGCGAAGGTGATGAGGTACAGGAGAGAGG 468  
 QY 158 LysArgArgArgTyfAspLysGlnIleArgTyfGluSerArgLysAlaTyfAlaGluLeu 177  
 DB 469 AAGAGCGGTGCTATGACAAGCAAAATCCGCTATGATGCCAGAAAGCTTACGCCGAGCTC 528  
 QY 178 ArgProArgValAsnGlyArgPheValLys 187  
 DB 529 AGGCCACGCGTCATGCGCGCTTTGTCAAG 558

RESULT 8  
 ADS19580  
 ID ADS19580 standard; DNA; 2913 BP.  
 XX  
 AC ADS19580;  
 DT 30-DEC-2004 (first entry)  
 XX  
 DE Langdon (tetraploid) wheat ZCCT1 genomic DNA.  
 XX  
 KW Wild emmer wheat; ds; APETALA1; AP1; vernalisation; flowering; ZCCT1;  
 XX ZCCT2; vrn1; vrn2; CARG box; plant; gene.  
 OS Triticum turgidum; subsp. dicoccoides.  
 XX  
 PN US2004205848-A1.  
 XX  
 PD 14-OCT-2004.  
 XX  
 PF 26-NOV-2003; 2003US-00723947.  
 XX  
 PR 11-APR-2003; 2003US-00412137.  
 XX (REGC ) UNIV CALIFORNIA.  
 PA Dubcovsky J, Yan L, Loukoianov A;  
 PI WPI: 2004-728059/71.  
 DR P-PSDB; ADS19582.  
 XX  
 PT New recombinant ZCCT1 protein coding sequence useful for altering a  
 PT plant's (e.g., wheat, barley, rye, oats, or forage grasses) response to  
 PT vernalization or flowering times.  
 XX  
 PS Disclosure; SEQ ID NO 78; 115pp; English.  
 XX  
 CC The invention relates to a recombinant ZCCT1 protein (Zn finger and CCT  
 CC domain protein) coding sequence comprising a nucleic acid that hybridises  
 CC to the barley ZCCT1 cDNA appearing as ADS19577. The patent also discloses  
 CC the identification of to genes, vrn1 identified as AP1 (APETALA1) and  
 CC vrn2 identified as ZCCT1 controlling vernalisation of flowering in  
 CC temperate grasses. ZCCT1 also has a duplicate gene ZCCT2, all three genes  
 CC have been localised to chromosome 5a of one grained wheat, Triticum  
 CC monococcum. ZCCT1 is the repressor of AP1 whose promoter contains a  
 CC binding site for ZCCT1 termed the CARG box. Also included are a vector  
 CC comprising the recombinant ZCCT1 protein coding sequence above, a cell  
 CC comprising the vector, a transgenic plant comprising the recombinant  
 CC ZCCT1 protein coding sequence above (or a genetic construct that inhibits  
 CC ZCCT1 repression of AP1), a seed from the transgenic plant, a method for  
 CC altering a plant's response to vernalisation and a molecular marker for

CC Vrn2 derived from ADS19577. The genetic construct is an interference RNA  
CC construct (RNAi) that inhibits ZCCT1 activity and comprises an antisense  
CC construct that inhibits ZCCT1 activity, a nucleic acid sequence encoding  
CC a repression defective ZCCT1 protein operably linked to a promoter or a  
CC nucleic acid sequence encoding a DNA binding defective ZCCT1 protein  
CC operably linked to a promoter. The present sequence is a plant ZCCT  
CC genomic DNA sequence.

XX SQ Sequence 2913 BP; 867 A; 627 C; 575 G; 844 T; 0 U; 0 Other;

## Alignment Scores:

Pred. No.:	1,01e-51	Length:	2913
Score:	670.50	Matches:	168
Percent Similarity:	28.3%	Conservative:	3
Best Local Similarity:	27.8%	Mismatches:	9
Query Match:	64.0%	Indels:	424
DB:	13	Gaps:	2

US-10-723-947-77 (1-187) x ADS19580 (1-2913)

Qy	1	MetSerMetSerCysGlyLeuCysGlyAlaAsnAsnCysProArgLeuMetValSerPro	20
Db	578	ATGTCCATGTCATGCGGTTGTGCGCGCCCAACAACTGCGCGCCTCATGTCTCGGCC	637
Qy	21	IleHisHisHisHisHisHisHisGlnGlnHisGlnLeuCysGluTyrGlnPhePheAla	40
Db	638	ATTTCATCATCGTCATCACCATCATCATCAGGAGCACCAGCTGCTCAGCACCAGTCTTCGCC	697
Qy	41	HisGlyAsnHisHisHisHisHisHisGlySerAlaAlaAspTyrProValProPro	60
Db	698	CAAGGCAACACACCACCACCAC-----CCAGTGCACCTGCCG	736
Qy	61	ProAspAsnPheAspHisArgThrTrpThrArgProPheHisGluThrAlaAlaAla	80
Db	737	CCAGCCAACTTCGACCATGACGAGAACATGACACACACCATTTTCATGAAACAGCAGCTGCA	796
Qy	81	GlyAsnSerSerArgLeuThrLeuGluValGlyAlaGlyGlyGlnHisMetAlaHisLeu	100
Db	797	GGGAACAGCAGCAGGCTCAGCTGGAGGTGGGCGCAGCGCGCCAGCCCATGGCTCACCTA	856
Qy	101	ValGlnProProAlaArgAlaHisIle-----	109
Db	857	GTGACGCCACCGGCAAGAGCCACATCGTAAGTAGTAGTACCGCTTAATGTTTTCATCTC	916
Qy	109	-----	109
Db	917	TTGCCGATGATGCGTCCCTGGCTTCTCTCTTAAABAATCCCCACCTAATTTATGTCATC	976
Qy	109	-----	109
Db	977	TATACCCACTACAAAAAATAGCACCATGTAAACCATTCATATATCTGTACATAATTCT	1036
Qy	109	-----	109
Db	1037	GTTAATGTAGCTGCTCAATGTTCTCTGAAAAAGATATGCGGGAATGGATCTTGATAT	1096
Qy	109	-----	109
Db	1097	TCCTTTAATTTCTATGGAGGCATATATAGAGTTTGTGTTTGTATTAGTTGACGAAT	1156
Qy	109	-----	109
Db	1157	TGTATGGGTTGTCAATCATCATCATATATATAAACTTATTTCATTTTATTGACCAAC	1216
Qy	109	-----	109
Db	1217	ACAAGGTAATCAGTCATACATCATGCTACTGAAAAATTTTGACTTGTGTTCAATAACTAACCA	1276
Qy	109	-----	109
Db	1277	ACTCGACCGGCACAGCTGGGGGAGACTTTAATCAAGCTGCTAGTAGAGCTTAATAATA	1336
Qy	109	-----	109

RESULT 9  
ADS19589

Db	1337	TAACATATCTCTTTATGGGATCAAGCAATACATATGCGCTCAATTCTCAACTTGTCAATA	1396
Qy	109	-----	109
Db	1397	TCATCTGGAGTCCACACTTTATGTAATTAATTCACAAAGTTTTGTGAAATGGACAATA	1456
Qy	109	-----	109
Db	1457	TACATACTGGATCGATGCAACCCTTTTCTCATTTTATGTGGTCAATTATGAATTTGATTCT	1516
Qy	109	-----	109
Db	1517	TATTTAGTATTCAATTTTATCTTGAGCTAGTTTTCGAAGTCTGTAGCTCATATATACT	1576
Qy	109	-----	109
Db	1577	GATACTACTCCCACGATAGCTTGGCTAGTGCGCGGTGATCGATCTACCGAGTTTCATAA	1636
Qy	109	-----	109
Db	1637	AACTGATCGAGATCGGTCCTCAAAAAAGAACAAACCCATACAAATGGAAGAGATCCTT	1696
Qy	109	-----	109
Db	1697	GTTTAGTTAGTTTGCATCAGAAAAATTCCTAATTAAGTTACTTGTCTATCAATCTTTTGAAC	1756
Qy	109	-----	109
Db	1757	ATGGCATGTTCACCCCAAACGGGACTCAGATCACAAATTATTGATGAAGTTACGCCTTTAA	1816
Qy	109	-----	109
Db	1817	AAACTCATAAAACTGTACATACATGTACAGGCTACACACATGTACATAATACACCTAAT	1876
Qy	109	-----	109
Db	1877	TAAACGTATATTCTGTAGACCAATTTGTTTGGACGGTGCCACATCTTTGAAAAAATGCC	1936
Qy	109	-----	109
Db	1937	AGAGGAGTTGTAGTTCCTCCACTGTCAGAAATAGATAGTTACAAATCAAGTGCATCTCTG	1996
Qy	109	-----	109
Db	1997	AATGAAAATGGATCATTTTCTAGTTAATTAGAGACCAATTAGATACTTTCATAAACAGGGG	2056
Qy	109	-----	109
Db	2057	AGTATCAAGTAGTATCTGTACTACCTAAGAAAGTACATACTGGCATCTTATGATTATTT	2116
Qy	110	-----ValProPheTyrGlyGlyAlaPheThrAsnThrIleSerAsnG1	124
Db	2117	TCCTCTTGATGTTCCAGGTGCCATTTTACGGAGGTGCATTTACCAACACATATTAGCAATCA	2176
Qy	124	uAlaIleMetThrIleAspThrGluMetMetValGlyProAlaHisTyrProThrMetG1	144
Db	2177	AGCAATCATGACTATTGACACAGAGATGATGTTGGGGCTGCGCCATTATCCCAATGCA	2236
Qy	144	nGluArgAlaAlaLysValMetArgTyrArgGluLysArgLysArgGlyArgTyrAspL1	164
Db	2237	GGAGAGACGACGAAGGTGATGAGGTATAGGGAAGAGAGAGGCGCGCTATGACAA	2296
Qy	164	sGlnIleArgTyrGluSerArgLysAlaTyrAlaGluLeuArgProArgValAsnGlyAr	184
Db	2297	GCAATCAGATACAGTCCAGAAAGCTTACGCTGAGCTTCGCGCCACCGGCTCAACGGCTG	2356
Qy	184	sPheValLys 187	
Db	2357	CTTTGTCAAG 2366	





Db 1470 TCATTGGACAAAGGCCCGGAAGTTGTTCTTCCATTGTCTAAATAAATAGAACAGT 1529  
Qy 109 ----- 109  
Db 1530 TACAGTCAAGTGCACACTGAATGAATGGATCAAGTTTGGTTAACAGAGACCAACT 1589  
Qy 109 ----- 109  
Db 1590 TATACCTTCATAAACAAGGAATATCAAGTACATATCTGTACCCACAAGAAAGTACACCT 1649  
Qy 110 ----- 120  
Db 1650 TATGACTATTTCTTCTTGTGATGTCAGGCGCATCTCGGAGAGTGTCATCCCGAGCACT 1709  
Qy 121 IleSerAsnGluAlaIleMetThrIleAspThrGluMetValGlyProAlaHisTyr 140  
Db 1710 ATTACCAAGCAACGATCATGACTATTGATACAGAAATGATGGTGGCGCTGCTATAT 1769  
Qy 141 ProThrMetGlnGluAlaAlaValMetArgTyrArgGluLysArgLysArg 160  
Db 1770 CCAACGATGCAGGAGAGAGCGAAGGTGATGAGGTACAGGAGAGAGAGAGGCGG 1829  
Qy 161 ArgTyrAspLysGlnIleArgTyrGluSerArgLysAlaTyrAlaGluLeuArgProArg 180  
Db 1830 CCCTATGACAAACAATCCGCTACGAGTCCAGAAAGCTTACGCCGAGCTCAGGCCAGG 1889  
Qy 181 ValAsnGlyArgPheValLys 187  
Db 1890 GTCAATGGCGCTTTGCCAAG 1910

## RESULT 10

ADSI19592  
ID ADSI19592 standard; DNA; 2043 BP.

AC ADSI19592;

XX 30-DEC-2004 (first entry)

DE Winter barley ZCCT-Hb genomic DNA.

KW Barley; ds; APETALA1; APL; vernalisation; flowering; ZCCT1; ZCCT2; vrn1;  
KW vrn2; CARG box; plant; gene.

XX Hordeum vulgare.

XX US2004205848-A1.

PD 14-OCT-2004.

XX 26-NOV-2003; 2003US-00723947.

XX 11-APR-2003; 2003US-00412137.

PA (REGC ) UNIV CALIFORNIA.

XX Dubcovsky J, Yan L, Loukoianov A;

XX WPI; 2004-728059/71.

DR P-PSDB; ADS19594.

XX New recombinant ZCCT1 protein coding sequence useful for altering a  
PT plant's (e.g., wheat, barley, rye, oats, or forage grasses) response to  
PT vernalization or flowering times.

PS Disclosure; SEQ ID NO 90; 115pp; English.

XX The invention relates to a recombinant ZCCT1 protein (Zn finger and CCT  
CC domain protein) coding sequence comprising a nucleic acid that hybridises  
CC to the barley ZCCT1 cDNA appearing as ADS19577. The patent also discloses  
CC the identification of to genes, vrn1 identified as APL (APETALA1) and  
CC vrn2 identified as ZCCT1 controlling vernalisation of flowering in  
CC temperate grasses. ZCCT1 also has a duplicate gene ZCCT2, all three genes  
CC have been localised to chromosome 5a of one grained wheat, Triticum

CC monococcum. ZCCT1 is the repressor of APL whose promoter contains a  
CC binding site for ZCCT1 termed the CARG box. Also included are a vector  
CC comprising the recombinant ZCCT1 protein coding sequence above, a cell  
CC comprising the vector, a transgenic plant comprising the recombinant  
CC ZCCT1 protein coding sequence above (or a genetic construct that inhibits  
CC ZCCT1 repression of APL), a seed from the transgenic plant, a method for  
CC altering a plant's response to vernalisation and a molecular marker for  
CC vrn2 derived from ADS19577. The genetic construct is an interference RNA  
CC construct (RNAi) that inhibits ZCCT1 activity and comprises an antisense  
CC construct that inhibits ZCCT1 activity, a nucleic acid sequence encoding  
CC a repressor defective ZCCT1 protein operably linked to a promoter or a  
CC nucleic acid sequence encoding a DNA binding defective ZCCT1 protein  
CC operably linked to a promoter. The present sequence is a plant ZCCT  
CC genomic DNA sequence.

SQ Sequence 2043 BP; 567 A; 495 C; 413 G; 527 T; 0 U; 41 Other;

## Alignment Scores:

Pred. No.:	6.95e-43	Length:	2043
Score:	572.50	Matches:	146
Percent Similarity:	30.3%	Conservative:	11
Best Local Similarity:	28.2%	Mismatches:	29
Query Match:	54.6%	Indels:	332
DB:	13	Gaps:	4

US-10-723-947-77 (1-187) x ADS19592 (1-2043)

Qy	1	MetSerMetSerCysGlyLeuCysGlyAlaAsnAsnCysProArgLeuMetValSerPro	20
Db	420	ATGTCATGGCATGGGTTTGTGGCGCCGACAAATGGCCGATCATCATGATGTCGCC	479
Qy	21	IleHisHisHisHisHisHisGlnGlnHisGlnLeuCysGluTyrGlnPheAla	40
Db	480	GTTCCTCTTCATCATCACCATCATCAGGAACATCGCAGCGCGAGTACAGTCTTCGCC	539
Qy	41	HisGlyAsnHisHisHisHisHisHisGlySerAlaAlaAspTyrProValPro	59
Db	540	CAAGGT---CACCAACACCCACCCAGCGCGCAGCAGCTACCCACCCGACAGCA	596
Qy	60	ProProAspAsnPheAspHisArgThrTrpThrArgProPheHisGluThrAlaAla	79
Db	597	CCGCGGCCCAATTCGCCACCCGCGCAGATCATGGCCAGCGCTTTCATGAAACAGCAGT	656
Qy	80	AlaGlyAsnSerSerArgLeuThrLeuGluValGlyAlaGlyGlyGlnHisMetAlaHis	99
Db	657	CCAGTGAATAGCACAGGCTCACAAAGAGGTGGACGCGCGCGCCACACAGATGCTCAC	716
Qy	100	LeuValGlnProProAla-Arg	106
Db	717	CTGCTGCAGCCACCGCGCGCGCCCAAGAGCCACCATCGTGAGTACTACTGCTTAATCGTTC	776
Qy	106	-----	106
Db	777	CATCTCTCCCGATCGATGTGACTCTCTTCTTAACAAAATACACACTTCTTCTTAATTCATC	836
Qy	106	-----	106
Db	837	TCAAAAAAAGCTAGCGCCATGTGACAGCTCATATATCTGTACATACTCCGTTAATTT	896
Qy	106	-----	106
Db	897	ATGCTGGTCGATTGTAATTTTACCAGGAGGAGAAAGTTTGTGTGTATCAGTTGATGCAC	956
Qy	106	-----	106
Db	957	AAGACTGGATGCTCAGATCATCAGTCACACATCATATATATTTATTTTATTTTTCATG	1016
Qy	106	-----	106
Db	1017	TAACAAGTAATCAGTTAATTCCTTTTATGGGGTCAAGCAACATATGTCCAGCCTTCATG	1076
Qy	106	-----	106

Db 1077 TTAATTCCTTGGCAGAGTTTGTGAATANAAGATATATATTGGATCAATGCACCCTACC 1136  
Qy 106 ----- 106  
Db 1137 TCTTCTCATTTTATGTGNCATTTAAATAATTTGAATGCTATTTTGTATTAATTTCTC 1196  
Qy 106 ----- 106  
Db 1197 NTGAGCTAGTTGNGAAGCTTATAGCTCAATTTAACTGGAANNNNNNNNNNNNNNNN 1256  
Qy 106 ----- 106  
Db 1257 NNNNNNNCGAGTTTCATGAACTGATCAAGATCAGTNCAAAANAGGCCAAACCTCNCGA 1316  
Qy 106 ----- 106  
Db 1317 AATGGAATTNCGATCCTTGTTAANTAGTTTGCATCAGGAATNGGCTACTTAATTAATTG 1376  
Qy 106 ----- 106  
Db 1377 CTACCAATNTATGAAGATGGCATGTTCTCTCACAATGATCCAGCTCACAATTTTGG 1436  
Qy 106 ----- 106  
Db 1437 TGAAGTTAAACATTTTGTAGCAATTCATAAAAGGTGCATAGATGTACAGGGCTACAGTAC 1496  
Qy 107 ----AlaHis----- 108  
Db 1497 ACAGGCACATAATACCGCTAGTTAAACATATATGATGAGCAATTTGAGTTGGACAAT 1556  
Qy 108 ----- 108  
Db 1557 GCGCTTCTTGGACATAATGGCCCGGAAATGTTCTCTCTCCATTGCTTAAAAACATAGA 1616  
Qy 108 ----- 108  
Db 1617 ACAGTTAGAATCAAGTGCACCACTGAATGAGATGGTCAATTTTGGTTAACGAGAGAC 1676  
Qy 109 -----IleVal 110  
Db 1677 CAACTATACGTTATAAACACTGCTACTCTCACCATTGTTTCTCTCTCGATGTTCCAGT 1736  
Qy 110 lProPheTyrGlyGlyAlaPheThrAsnThrIleSerAsnGluAlaIleMetThrIleAs 130  
Db 1737 GCAATTCGCCGGAGTGCAATTCACCAACTATTAGCAACGCAACGATCATGACTATTGA 1796  
Qy 130 pThrGluMetMetValGlyProAlaHisTyrProThrMetGlnGluArgAlaAlaLysVa 150  
Db 1797 TACAGAGATGATGGCGGGGACTGCCTATAGTCCACGATGCAGGAAAGAGAAAGT 1856  
Qy 150 lMetArgTyrArgGluLysArgLysArgArgTyrAspLysGlnIleArgTyrGluSe 170  
Db 1857 GATGAGGTACAGGAGAGAGGAAGGCGGCTATGACAAGCAATCCGCTACGAGTC 1916  
Qy 170 rArgLysAlaTyrAlaGluLeuArgProArgValAsnGlyArgPheValLys 187  
Db 1917 CAGAAAGCTTACGCCGAGCTTAGGCCACGGGTCAACGCCGCTTTGTCAAG 1968  
RESULT 11  
ID ADS19583 standard; DNA; 5734 BP.  
XX ADS19583;  
AC ADS19583;  
XX 30-DEC-2004 (first entry)  
DT One grained wheat DV92 ZCCT2 genomic DNA.  
DE One grained wheat; chromosome 5a; ds; APETAL1; AP1; vernalisation;  
KW flowering; ZCCT1; ZCCT2; vrnl; vrn2; CARG box; plant; gene.  
XX Triticum monococcum.  
OS

PN US2004205848-A1.  
XX 14-OCT-2004.  
PF 26-NOV-2003; 2003US-00723947.  
XX 11-APR-2003; 2003US-00412137.  
XX (REGC ) UNIV CALIFORNIA.  
PA Dubcovsky J, Yan L, Loukoianov A;  
PI WPI; 2004-728059/71.  
XX P-PSDB; ADS19585.  
PT New recombinant ZCCT1 protein coding sequence useful for altering a  
PT plant's (e.g., wheat, barley, rye, oats, or forage grasses) response to  
PT vernalization or flowering times.  
XX Disclosure; SEQ ID NO 81; 115pp; English.  
XX The invention relates to a recombinant ZCCT1 protein (Zn finger and CCT  
XX domain protein) coding sequence comprising a nucleic acid that hybridises  
XX to the barley ZCCT1 cDNA appearing as ADS19577. The patent also discloses  
XX the identification of to genes, vrnl identified as AP1 (APETAL1) and  
XX vrn2 identified as ZCCT1 controlling vernalisation of flowering in  
XX temperate grasses. ZCCT1 also has a duplicate gene ZCCT2, all three genes  
XX have been localised to chromosome 5a of one grained wheat, Triticum  
XX monococcum. ZCCT1 is the repressor of AP1 whose promoter contains a  
XX binding site for ZCCT1 termed the CARG box. Also included are a vector  
XX comprising the recombinant ZCCT1 protein coding sequence above, a cell  
XX comprising the vector, a transgenic plant comprising the recombinant  
XX ZCCT1 protein coding sequence above (or a genetic construct that inhibits  
XX ZCCT1 repression of AP1), a seed from the transgenic plant, a method for  
XX altering a plant's response to vernalisation and a molecular marker for  
XX Vrnl derived from ADS19577. The genetic construct is an interference RNA  
XX construct (RNAi) that inhibits ZCCT1 activity and comprises an antisense  
XX construct that inhibits ZCCT1 activity, a nucleic acid sequence encoding  
XX a repressor defective ZCCT1 protein operably linked to a promoter or a  
XX nucleic acid sequence encoding a DNA binding defective ZCCT1 protein  
XX operably linked to a promoter. The present sequence is a plant ZCCT  
XX genomic DNA sequence.  
SQ Sequence 5734 BP; 1563 A; 1278 C; 1220 G; 1673 T; 0 U; 0 Other;  
Alignment Scores:  
Pred. No.: 4,936-40 Length: 5734  
Score: 547.50 Matches: 145  
Percent Similarity: 28.2% Conservative: 11  
Best Local Similarity: 26.2% Mismatches: 27  
Query Match: 52.2% Indels: 371  
DB: 13 Gaps: 5  
US-10-723-947-77 (1-187) x ADS19583 (1-5734)  
Qy 1 MetSerMetSerCysGlyLeuCysGlyAlaAsnAsnCysProArgLeuMetValSerPro 20  
Db 2589 ARGTCATGTCATGCGGTTTGTGCGCGCAAGCACTGCCCCACCAATGATCTCGCCC 2648  
Qy 21 IleHisHisHisHisHisHisGlnGluHisGlnLeuCysGlyTyrGlnPhePheAla 40  
Db 2649 GTT-----CTTCAGCATCAGGAACAACACTGGCTGCGGAGTACCAGTCTTCACC 2699  
Qy 41 HisGlyAsnHisHisHisHisHisGlySerAlaAlaAspTyrProValProProPro 60  
Db 2700 CAAGGC---CACCACCAACCAACCGCGCGCGGAGTACCCACCGCCACCGCCA 2756  
Qy 61 ProAsp---AsnPheAspHisArgThrTrpThrArgProPheHisGluThrAlaAla 79  
Db 2757 CGTCGCGCAATTTGCCACCACTGCATGAGTACCAACCCGTTTCATGAACAGCAGCT 2816  
Qy 80 AlaGlyAsnSerSerArgLeuThrLeuGluValGlyAlaGlyGlnHisMetAlaHis 99



CC construct that inhibits ZCCT1 activity, a nucleic acid sequence encoding  
CC a repression defective ZCCT1 protein operably linked to a promoter or a  
CC nucleic acid sequence encoding a DNA binding defective ZCCT1 protein  
CC operably linked to a promoter. The present sequence is a plant ZCCT  
CC genomic DNA sequence.

Qy	109	-----	109
Db	2071	AAGTATAACAGATACTACTCCCATTAATTGCTTCCGTAGTGGCGGTGATCAATCTACC	2130
Qy	109	-----	109
Db	2131	GAGTTCATAAACTGATCGAATCAGATCCAAAACAGACCAAAACCTCAGGAATAGAAA	2190
Qy	109	-----	109
Db	2191	CAAGATCCTTGTTTAATTAGTTTGACACAGGAATTCCTACTTAATTACTTTCTATCAA	2250
Qy	109	-----	109
Db	2251	TCATTATGAAGATGGTATGTTTCTCACATATGGTGATCCAGATCACAATTGTTGACGGAGT	2310
Qy	109	-----	109
Db	2311	TAAACATTTTAGCAATTTCATAAAACCGTGACAGATGTACAGGGCTACCGGTATGCACA	2370
Qy	109	-----	109
Db	2371	TACATAATACACCTAATTAACAATATATTCATAGAGCGATTGAGTTTGGACTGTGCGCT	2430
Qy	109	-----	109
Db	2431	TCTTTGGACACAAAGCCCGGGAAGTTGTTCTCTTCATGCTAGAAAAATAGAACAGT	2490
Qy	109	-----	109
Db	2491	TACAATCAAGTGCACCACCTGAATGAAATGGGTCAATTCTGGTTAATAAGAGACCAACTG	2550
Qy	109	-----	109
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Qy	110	-----ValProPheTyrGlyGlyAlaPheTh	118
Db	2611	GCACCTTAGGATTATTTCTCTTCATGTTCCAGTGCCTTCTGCGGGGCTGCATTCAC	2670
Qy	118	rAsnThrIleSerAsnGluAlaIleMetThrIleAspThrGluMetMetValGlyProAl	138
Db	2671	CAGCACTATTAGCAATGCAACGATCATGACTATTGATACAGAGATGATGTTGGGGCTGC	2730
Qy	138	aHisTyrProThrMetGlnGluArgAlaAlaIysValMetArgTyrArgGluIysArgLy	158
Db	2731	CCATAATCTGACGATCGACGAGAGAGGCGAAGGTGATGAGGTACAGGGAAGAGGAA	2790
Qy	158	sArgAspArgTyrAspLysGlnIleArgTyrGluSerArgLysAlaTyrAlaGluLeuAr	178
Db	2791	GAGCGGTGCTATGACAGCAAAATCGCTATGAGTCCAGAAAGCTTACGCCGAGGTCCAG	2850
Qy	178	gProArgValAsnGlyArgPheValIys	187
Db	2851	GCCACCGGTCAATGGCGCTTTGTCAAG	2878





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Qy      89 GluValGlyAlaGlyGlyGlnHisMetAlaHisLeuValGlnProProAlaArgAlaHis 108
Db      :::| | | | |
600 GGGCTCGGCTCGGCGCGGCGGCGGCAC---GCCGAGCGCGCGCCAGCGCCACC 656
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Db      | | | | |
657 ATCATGTCATATTGTGGGAGCAGCTTCACTGACGCGAGCGAGCTCGATGCCCAAGGAGATG 716
Qy      129 IleAspThrGluMetMetValGlyProAlaHisTyrPro-----ThrMet 143
Db      | | | | |
717 GTGCCCGCCATGGCCGATGTTGGGAGAGCTTGAACCCAAACACGCGTGTGGCGCAATG 776
Qy      144 GlnGluArgAlaAlaLysValMetArgTyrArgGluLysArgLysArgArgTyrAsp 163
Db      | | | | |
777 GTGGAGAGGAGGCCCAAGCTGATGAGGTACAAGGAGAGAGGAAGAGGTGCTACCGAG 836
Qy      164 LysGlnIleArgTyrGluSerArgLysAlaTyrAlaGluLeuArgProArgValAsnGly 183
Db      | | | | |
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Qy      184 ArgPheValLys 187
Db      | | | | |
897 CGCTTCGCCCAA 908
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Search completed: February 23, 2006, 11:04:32  
Job time : 502 secs

GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model.

Run on: February 23, 2006, 10:36:58 ; Search time 4542 Seconds  
(without alignments)  
2340.318 Million cell updates/sec

Title: US-10-723-947-77

Perfect score: 1048

Sequence: 1 MSMSGCLGANNCPRLMVSP.....YESRKAYAEPRVNGRFVK 187

Scoring table: BLOSUM62

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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

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Database :

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2: gb.in.\*  
3: gb.env.\*  
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10: gb.sts.\*  
11: gb.sy.\*  
12: gb.un.\*  
13: gb.vi.\*  
14: gb.htg.\*  
15: gb.pl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1048	100.0	792	15	AY485969 Triticum
2	1048	100.0	850	15	AY485963 Triticum
3	1043	99.5	850	15	AY485965 Triticum

	4	1043	99.5	850	15	AY485966	Triticum
	5	1043	99.5	850	15	AY485968	Triticum
	6	1039	99.1	850	15	AY485967	Triticum
	7	1018.5	97.2	847	15	AY485964	Triticum
C	8	816	77.9	110000	15	AY485964_3	Continuation (4 of
	9	730.5	69.7	712	15	AY485975	AY485975 Triticum
	10	730.5	69.7	712	15	AY485976	AY485975 Triticum
	11	670.5	64.0	2078	15	AY485979	AY485979 Triticum
	12	590	56.3	1985	15	AY485977	AY485977 Hordeum v
	13	569	54.3	2064	15	AY485978	AY485978 Hordeum v
C	14	547.5	52.2	110000	15	AY485964_2	Continuation (3 of
	15	538	51.3	1790	15	AY485980	AY485980 Triticum
	16	260	24.8	264	15	AY687931	AY687931 Hordeum v
	17	247.5	23.6	1258	15	AK109732	AK109732 Oryza sat
	18	207	19.8	1068	6	CQ804432	Sequence
	19	207	19.8	1099	15	AY114006	AY114006 Arabidops
	20	207	19.8	1305	15	AY057632	AY057632 Arabidops
	21	207	19.8	1377	15	AY088432	AY088432 Arabidops
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	24	200.5	19.1	144191	15	AC079874	AC079874 Oryza sat
C	25	200.5	19.1	300029	15	AE017119	AE017119 Oryza sat
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	27	195.5	18.7	110000	15	AP008208_240	Continuation (241
	28	195.5	18.7	125426	15	AP004063	Continuation (241
	29	194	18.5	1386	15	AK100097	AP004063 Oryza sat
	30	194	18.5	1388	15	AK058536	AK058536 Oryza sat
	31	193	18.4	1056	15	AY082963	AY082963 Hordeum v
	32	191.5	18.3	50700	15	AB018118	AB018118 Arabidops
	33	190.5	18.2	1324	15	AY082962	AY082962 Hordeum v
	34	190.5	18.2	1455	15	AY082961	AY082961 Hordeum v
	35	188.5	18.0	110000	15	AP008213_091	Continuation (92 o
C	36	188.5	18.0	150554	15	AP005307	AP005307 Oryza sat
	37	188	17.9	1101	6	AS0834	AS0834 Sequence
	38	188	17.9	1101	6	AR099794	AR099794 Sequence
	39	187.5	17.9	944	15	AY082965	AY082965 Hordeum v
	40	187	17.8	1163	15	AY082960	AY082960 Hordeum v
	41	185.5	17.7	1370	15	AK109630	AK109630 Oryza sat
	42	183	17.5	1060	15	AY082958	AY082958 Hordeum v
	43	182.5	17.4	966	15	AY496442	AY496442 Brassica
	44	182.5	17.4	1085	15	AF490474	AF490474 Hordeum v
	45	182	17.4	966	15	AY356370	AY356370 Brassica

#### ALIGNMENTS

RESULT 1	AY485969	792 bp	mRNA	linear	PLN 17-MAR-2004
LOCUS	Triticum monococcum cultivar G3116 ZCCT1 (VRN2)	mRNA	linear	PLN 17-MAR-2004	
DEFINITION	Triticum monococcum cultivar G3116 ZCCT1 (VRN2) mRNA, complete cds.				
ACCESSION	AY485969				
VERSION	AY485969.1	GI:45390705			
KEYWORDS	Triticum monococcum				
SOURCE	Triticum monococcum				
ORGANISM	Triticum monococcum				
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;				
AUTHORS	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;				
	Pooideae; Triticeae; Triticum.				
	1 (bases 1 to 792)				
	SanMiguel, P., Bennetzen, J.L., Echenique, V. and Dubcovsky, J.				
	The Wheat VRN2 Gene Is a Flowering Repressor Down-Regulated by				
	Vernalization				
	Science 303 (5664), 1640-1644 (2004)				
	15016992				
	2 (bases 1 to 792)				
	SanMiguel, P., Bennetzen, J.L., Echenique, V. and Dubcovsky, J.				
	Yan, L., Loukianov, A., Blechl, A., Tranquillini, G., Ramakrishna, W.,				
	SanMiguel, P., Bennetzen, J.L., Echenique, V. and Dubcovsky, J.				
	Direct Submission				
	Submitted (20-NOV-2003) Agronomy and Range Science, University of				
	California, One Shields Avenue, Davis, CA 95616, USA				
	Location/Qualifiers				
	1. .792				



RESULT 2  
AY485963

QY 81 GlyAsnSerArgLeuThrLeuGluValGlyAlaGlyGlnHisMetAlaHisLeu 100  
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 Db 396 GTGAGCCACCGGCAAGAGCCACATCGTGCCATTTTACGGAGGTGCATTACCAACACT 455  
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 QY 121 IleSerAsnGluAlaIleMetThrIleAspThrGluMetMetValGlyProAlaHisTyr 140  
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 QY 161 ArgTyrAspGlyGlnIleArgTyrGluSerArgLysAlaTyrAlaGluLeuArgProArg 180  
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 Db 576 CGCTATGACAAGCAATCCATACGAGTCCAGAAAGCTTACGCTGAGCTCGGCGCAGG 635  
 |||||  
 QY 181 ValAsnGlyArgPheValLys 187  
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 Db 636 GTCAACGGCGCTTTGTCAAG 656  
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 RESULT 3  
 LOCUS AY485965 850 bp mRNA linear PLN 17-MAR-2004  
 DEFINITION Triticum monococcum cultivar PI272561 ZCCT1 (VRN2) mRNA, complete cds.  
 ACCESSION AY485965  
 VERSION AY485965.1 GI:45390685  
 KEYWORDS Triticum monococcum  
 SOURCE Triticum monococcum  
 ORGANISM Triticum monococcum  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Poideae; Triticeae; Triticum.  
 1 (bases 1 to 850)  
 Yan, L., Loukoianov, A., Blechl, A., Tranquilli, G., Ramakrishna, W.,  
 SanMiguel, P., Bennetzen, J.L., Echenique, V. and Dubcovsky, J.  
 The Wheat VRN2 Gene Is a Flowering Repressor Down-Regulated by  
 Vernalization  
 Science 303 (5664), 1640-1644 (2004)  
 15016992  
 2 (bases 1 to 850)  
 Yan, L., Loukoianov, A., Blechl, A., Tranquilli, G., Ramakrishna, W.,  
 SanMiguel, P., Bennetzen, J.L., Echenique, V. and Dubcovsky, J.  
 Submitted (20-NOV-2003) Agronomy and Range Science, University of  
 California, One Shields Avenue, Davis, CA 95616, USA  
 Location/Qualifiers  
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 Db 96 ATGTCCATGTCTATGGTTTGTGGCGGCCAACAACTGCCCCGCTCATGCTCTCGCC 155  
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 QY 21 IleHisHisHisHisHisHisHisGlnGlnHisGlnLeuCysGluTyrGlnPhePheAla 40  
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 Db 156 ATTCAACCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 215  
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 QY 41 HisGlyAsnHisHisHisHisHisHisHisGlySerAlaAlaAspTyrProValProPro 60  
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 QY 61 ProAspAsnPheAspHisArgArgThrTrpThrArgProPheHisGluThrAlaAlaAla 80  
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 Db 276 CCAGACAACTTCGACCAACCGCAGAACATGGACCAACCACTTCATGAAACAGCAGCGCA 335  
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 QY 81 GlyAsnSerArgLeuThrLeuGluValGlyAlaGlyGlnHisMetAlaHisLeu 100  
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 Db 336 GGGAAAGCAGCAGAGGCTCAGCTGGAGGTGGCGCGCAGCGCCAAACACATGGCTCACCTA 395  
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 QY 141 ProThrMetGlnGluAlaAlaLysValMetArgTyrArgGluLysArgLysArgArg 160  
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 QY 161 ArgTyrAspGlyGlnIleArgTyrGluSerArgLysAlaTyrAlaGluLeuArgProArg 180  
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 QY 181 ValAsnGlyArgPheValLys 187  
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 Db 636 GTCAACGGCGCTTTGTCAAG 656  
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 RESULT 4  
 LOCUS AY485966 850 bp mRNA linear PLN 17-MAR-2004  
 DEFINITION Triticum monococcum cultivar PI573529 ZCCT1 (VRN2) mRNA, complete cds.  
 ACCESSION AY485966  
 VERSION AY485966.1 GI:45390690  
 KEYWORDS Triticum monococcum  
 SOURCE Triticum monococcum  
 ORGANISM Triticum monococcum  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Poideae; Triticeae; Triticum.  
 1 (bases 1 to 850)  
 Yan, L., Loukoianov, A., Blechl, A., Tranquilli, G., Ramakrishna, W.,  
 SanMiguel, P., Bennetzen, J.L., Echenique, V. and Dubcovsky, J.  
 The Wheat VRN2 Gene Is a Flowering Repressor Down-Regulated by  
 Vernalization  
 Science 303 (5664), 1640-1644 (2004)  
 15016992  
 2 (bases 1 to 850)  
 Yan, L., Loukoianov, A., Blechl, A., Tranquilli, G., Ramakrishna, W.,  
 SanMiguel, P., Bennetzen, J.L., Echenique, V. and Dubcovsky, J.

Dbb 636 GTCAACGGCGCTTTGTCAAG 656

|||||

RESULT 5  
AY485968 850 bp mRNA linear PLN 17-MAR-2004  
LOCUS Triticum monococcum cultivar PI355532 ZCCT1 (VRN2) mRNA, complete cds.  
DEFINITION AY485968.1 GI:45390700  
ACCESSION AY485968  
VERSION  
KEYWORDS  
SOURCE Triticum monococcum  
ORGANISM Triticum monococcum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Pooideae; Triticeae; Triticum.  
REFERENCE 1 (bases 1 to 850)  
AUTHORS Yan,L., Loukoianov,A., Blechl,A., Tranquilli,G., Ramakrishna,W.,  
SanMiguel,P., Bennettzen,J.L., Echenique,V. and Dubcovsky,J.  
TITLE The Wheat VRN2 Gene Is a Flowering Repressor Down-Regulated by  
Vernalization  
JOURNAL Science 303 (5664), 1640-1644 (2004)  
PUBMED 15016992  
REFERENCE 2 (bases 1 to 850)  
AUTHORS Yan,L., Loukoianov,A., Blechl,A., Tranquilli,G., Ramakrishna,W.,  
SanMiguel,P., Bennettzen,J.L., Echenique,V. and Dubcovsky,J.  
TITLE Direct Submission  
JOURNAL Submitted (20-NOV-2003) Agronomy and Range Science, University of  
California, One Shields Avenue, Davis, CA 95616, USA  
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ORIGIN

Alignment Scores:	
Pred. No.:	1.9e-68
Score:	Length: 850
Percent Similarity:	Matches: 186
Best Local Similarity:	Conservative: 1
Query Match:	Mismatches: 0
DB:	Indels: 0
	Gaps: 0

US-10-723-947-77 (1-187) x AY485968 (1-850)

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Qy 21 ILGHISHISHISHISHISHIGHISGLIUHISGLIeuCysGLUTyrGlnPhePheAla 40

Db 156 ATTACCATTATCATCACCATCATCATAGGAGCACAGCTGTGTGAGTACCAAGTTCTTCGCC 215

Qy 41 HIGLYAnSHISHISHISHISHISHIGHISGLYSerAlaAlaaspYrProValProPro 60

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QY 61 ProAspAsnPheAspHisArgThrTrrThrArgProPheHisGluThrAlaAla 80
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QY 161 ArgTyrAspLysGlnIleArgTyrGluSerArgLysAlaTyrAlaGluLeuArgProArg 180
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QY 181 ValAsnGlyArgPheValLys 187
DB 636 GTCACCGCGCGCTTGTCAAG 656

RESULT 6
LOCUS AY485967 850 bp mRNA linear PLN 17-MAR-2004
DEFINITION Triticum monococcum cultivar PI221413 ZCCT1 (VRN2) mRNA, complete cds.
ACCESSION AY485967
VERSION AY485967.1 GI:45390695
KEYWORDS Triticum monococcum
SOURCE Triticum monococcum
ORGANISM Triticum monococcum
REFERENCE 1 (bases 1 to 850)
AUTHORS Yan, L., Loukianov, A., Blechl, A., Tranquilli, G., Ramakrishna, W., San Miguel, P., Bennett, J. L., Echenique, V., and Dubcovsky, J.
TITLE The Wheat VRN2 Gene Is a Flowering Repressor Down-Regulated by Vernalization
JOURNAL Science 303 (5664), 1640-1644 (2004)
PUBMED 15016992
REFERENCE 2 (bases 1 to 850)
AUTHORS Yan, L., Loukianov, A., Blechl, A., Tranquilli, G., Ramakrishna, W., San Miguel, P., Bennett, J. L., Echenique, V., and Dubcovsky, J.
TITLE Direct Submission
JOURNAL Submitted (20-NOV-2003) Agronomy and Range Science, University of California, One Shields Avenue, Davis, CA 95616, USA
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ORIGIN
Alignment Scores: 3.75e-68 Length: 850
Pred. No.: 1039.00 Matches: 185
Percent Similarity: 100.0% Conservative: 2
Best Local Similarity: 98.9% Mismatches: 0
Query Match: 99.1% Indels: 0
DB: 15 Gaps: 0

US-10-723-947-77 (1-187) x AY485967 (1-850)
QY 1 MetSerMetSerCysGlyLeuCysGlyAlaAsnAsnCysProArgLeuMetValSerPro 20
DB 96 ATGTCATCATCGCTGCGGTTTGTGCGCGCCCAACACTGCCGCGCTCATGGTCTCGCCC 155
QY 21 IleHisHisHisHisHisHisHisHisHisHisHisHisHisHisHisHisHisHis 40
DB 156 ATTACCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 215
QY 41 HisGlyAsnHisHisHisHisHisHisHisHisHisHisHisHisHisHisHisHisHis 60
DB 216 CATGCAACCCACCCACCCACCCACCCACCCACCCACCCACCCACCCACCCACCCAC 275
QY 61 ProAspAsnPheAspHisArgThrTrrThrArgProPheHisGluThrAlaAlaAla 80
DB 276 CCAGACAACTTCACCAACCCAGCAACATGACCAAGCAATTCATGAACAGCAGCGCA 335
QY 81 GlyAsnSerSerArgLeuThrLeuGluValGlyAlaGlyGlyGlnHisMetAlaHisLeu 100
DB 336 GGGAAACAGCAGCAGCGGTTCACGCTGGAGGTGGCGCGCAGCGCCCAACACATGGCT 395
QY 101 ValGlnProProAlaAlaHisIleValProPheThrGlyGlyAlaPheThrAsnThr 120
DB 396 GTCACGCCACCGCAAGAGCCCAATCGTCCCAATTCACGGAGGTGATTCACCAACACT 455
QY 121 IleSerAsnGluAlaIleMetThrIleAspThrGluMetMetValGlyProAlaHisTyr 140
DB 456 ATTAGCAATGAACCAATCATGACTATTGACACAGAGATGATGGTGGGCTGCCCATAT 515
QY 141 ProThrMetGlnGluAlaAlaLysValMetArgTyrArgGluLysArgLysArg 160
DB 516 CCCACAATGACGAGAGAGCAGCGAAGGTGATGAGGTATAGGAGAGAGAGAGCGCG 575
QY 161 ArgTyrAspLysGlnIleArgTyrGluSerArgLysAlaTyrAlaGluLeuArgProArg 180
DB 576 CGCTATGACAAGCAATCCGATACGAGTCCAGAAAGCTTACGCTGAGCTTCGCCACCG 635
QY 181 ValAsnGlyArgPheValLys 187
DB 636 GTCACCGCGCGCTTGTCAAG 656

RESULT 7
LOCUS AY485964 847 bp mRNA linear PLN 17-MAR-2004
DEFINITION Triticum monococcum cultivar PI277133 ZCCT1 (VRN2) mRNA, complete cds.
ACCESSION AY485964
VERSION AY485964.1 GI:45390680
KEYWORDS Triticum monococcum
SOURCE Triticum monococcum
ORGANISM Triticum monococcum
REFERENCE 1 (bases 1 to 847)
AUTHORS Yan, L., Loukianov, A., Blechl, A., Tranquilli, G., Ramakrishna, W., San Miguel, P., Bennett, J. L., Echenique, V., and Dubcovsky, J.
TITLE The Wheat VRN2 Gene Is a Flowering Repressor Down-Regulated by Vernalization

```

JOURNAL Science 303 (5664), 1640-1644 (2004)  
PUBMED 15016992  
REFERENCE 2 (bases 1 to 847)  
AUTHORS Yan, L., Loukoianov, A., Blechl, A., Tranquilli, G., Ramakrishna, M.,  
SanMiguel, P., Bennetzen, J. L., Echenique, V. and Dubcovsky, J.  
TITLE Direct Submission  
JOURNAL Submitted (20-NOV-2003) Agronomy and Range Science, University of  
California, One Shields Avenue, Davis, CA 95616, USA  
FEATURES Location/Qualifiers  
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/db\_xref="taxon:4568"  
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1..847  
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96..734  
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ORIGIN  
Alignment Scores:  
Pred. No.: 1,23e-66 Length: 847  
Score: 1018.50 Matches: 184  
Percent Similarity: 98.9% Conservative: 1  
Best Local Similarity: 98.4% Mismatches: 1  
Query Match: 97.2% Indels: 1  
DB: 15 Gaps: 1  
US-10-723-947-77 (1-187) x AY485964 (1-847)

QY 161 ArgTyrAspLysGlnIleArgTyrGluSerArgLysAlaTyrAlaGluLeuArgProArg 180  
Db 573 CGCTATGACAAAGCAATCCGATACGAGTCCAGAAAGCTTACGCTGAGCTTCGGCCACGG 632  
QY 181 ValLengArgPheValLys 187  
Db 633 GTCAACGGCCGCTTTGTCAAG 653  
RESULT 8  
AY485644\_3/c  
WPCOMMENT  
Sequence split into 5 fragments LOCUS AY485644 Accession AY485644  
Fragment Name Begin End  
AY485644\_0 1 110000  
AY485644\_1 100001 210000  
AY485644\_2 210001 310000  
AY485644\_3 310001 410000  
AY485644\_4 410001 438828  
Continuation (4 of 5) of AY485644 from base 300001 (AY485644 Triticum monococcum phospho-  
putative transposase, phosphatidylinositol phospho.  
Alignment Scores:  
Pred. No.: 2,56e-49 Length: 110000  
Score: 816.00 Matches: 185  
Percent Similarity: 30.7% Conservative: 1  
Best Local Similarity: 30.6% Mismatches: 1  
Query Match: 77.9% Indels: 418  
DB: 15 Gaps: 1  
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Db 32804 ATGTCATGTCATGCGTTTGTGCGCGCCAACTGCCCGCCTCATGTGCTCGCC 32745  
QY 21 IleHisHisHisHisHisHisHisGlnGluHisGlnLeuCysGlyTyrGlnPhePheAla 40  
Db 32744 ATTCACCATCATCATCACCATCATCAGGAGCACCAGCTGTGTGAGTACCAGTTCTTCGCC 32685  
QY 41 HisGlyAsnHisHisHisHisHisHisGlySerAlaAlaAspTyrProValProPro 60  
Db 32684 CATGGCAACCCACCACCACCACCACCATGCTCGGAGAGACTACCCAGTGCACCGCCG 32625  
QY 61 ProAspAsnPheAspHisArgThrTrpThrArgProPheHisGluThrAlaAlaAla 80  
Db 32624 CCAGACAACTTCGACCAACCGCAGAACATGGACCAACATTTTCATGAAACAGCAGCGCA 32565  
QY 81 GlyAsnSerSerArgLeuThrLeuGluValGlyAlaGlyGlyGlnHisMetAlaHisLeu 100  
Db 32564 GGGAAACAGCAGCGCTCACGCTGGAGGTGGCGCAGCGGCCAACACATGGCTCACCTA 32505  
QY 101 ValGlnProAlaAlaAlaHisile 109  
Db 32504 GTGAGCCACCGGCAAGAGCCACATCTGTAAGTAGTACTACTGCTTAATTGTTTCATCTC 32445  
QY 109 109  
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QY 109 109  
Db 32384 TGACTACCCCACTACAAAAAGTAGCACCATTGTAACCATTTTCATATATTTCTCATATA 32325  
QY 109 109  
Db 32324 TTCGTGTTAATTACGCTGCTCGATTGTTCTCTCTGAAAGATATACGGAATGGATCTGG 32265  
QY 109 109  
Db 32264 ATATCTTTAATTTTCTATGAGGCGATAGAGTTTGTGTTTGTATTGATTGATGAGAAT 32205  
QY 109 109

Db 32204 TGTATGGGTTGTCAAATCATCATCATATATATATCTTATTTCTTTTGTGACCAAC 32145  
QY 109 ----- 109  
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QY 109 ----- 109  
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QY 109 ----- 109  
Db 32024 AATATAACATATCTCTTTATGGGATCAAGCAATACATATATCGCTCAATCTCAACTGTTC 31965  
QY 109 ----- 109  
Db 31964 AATATCTATCTGAGTCCACACTTTATGTAATTAATGACAAAGTTTGTGAAATGGAC 31905  
QY 109 ----- 109  
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QY 109 ----- 109  
Db 31844 GTTATTTAGTATTCAATTTTATCTTGTAGCTAGTTTGGCAAGTCTGTAGTCTATATAATA 31785  
QY 109 ----- 109  
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QY 109 ----- 109  
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QY 109 ----- 109  
Db 31664 TTGTTTAGTTAGTTTGCATCAGAAATTCGCTAATTAGTTTACCTGCTATCAATCTTTTGA 31605  
QY 109 ----- 109  
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QY 110 ----- ValProPheTyrGlyAlaPheThrAsnThrIleSer 122  
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QY 123 AsnGluAlaIleMetThrIleAspThrGluMetMetValGlyProAlaHisTyrProThr 142  
Db 31184 AATGAAGCAATCATGACTATTGACACAGAGATGATGTTGGGGCTTGCCTATATCCACA 31125  
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QY 163 AspLysGlnIleArgTyrGluSerArgLysAlaTyrAlaGluLeuArgProArgValAsn 182  
Db 31064 GACAAGCAATCCGATAGAGTCCAGAAAGCTTACGCTTCGGCCATCGGTCAC 31005  
QY 183 GlyArgPheValLys 187  
Db 31004 GGCCGCTTTGTCAAG 30990  
RESULT 9  
AY485975 712 bp mRNA linear PLN 17-MAR-2004  
LOCUS Triticum monococcum cultivar PI277133 ZCCT2 (VRN2) mRNA, complete  
DEFINITION cds.  
ACCESSION AY485975  
VERSION AY485975.1 GI:45390730  
KEYWORDS Triticum monococcum  
SOURCE Triticum monococcum  
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Poideae; Triticeae; Triticum.  
REFERENCE 1 (bases 1 to 712)  
AUTHORS Yan, L., Loukolanov, A., Blechl, A., Tranquilli, G., Ramakrishna, W.,  
SanMiguel, P., Bennett, J. L., Echenique, V. and Dubcovsky, J.  
TITLE The Wheat VRN2 Gene Is a Flowering Repressor Down-Regulated by  
Vernalization  
JOURNAL Science 303 (5664), 1640-1644 (2004)  
PUBMED 15016992  
REFERENCE 2 (bases 1 to 712)  
AUTHORS Yan, L., Loukolanov, A., Blechl, A., Tranquilli, G., Ramakrishna, W.,  
SanMiguel, P., Bennett, J. L., Echenique, V. and Dubcovsky, J.  
TITLE Direct Submission  
JOURNAL Submitted (20-NOV-2003) Agronomy and Range Science, University of  
California, One Shields Avenue, Davis, CA 95616, USA  
FEATURES  
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## ORIGIN

## Alignment Scores:

Pred. No.: 2,146-45 Length: 712  
Score: 730.50 Matches: 144  
Percent Similarity: 81.6% Conservative: 11  
Best Local Similarity: 75.8% Mismatches: 28  
Query Match: 69.7% Indels: 7  
DB: 15 Gaps: 4

US-10-723-947-77 (1-187) x AY485975 (1-712)

QY 1 MetSerMetSerCysGlyLeuCysGlyAlaAsnAsnCysProArgLeuMetValSerPro 20  
Db 29 ATGTCATGTCATGCGTTTGTGCGCGCAAGCAAGCTGCCCGCACCATGATCTCGCCC 88  
QY 21 IleHisHisHisHisHisHisGlnGluHisGlnLeuCysGluTyrGlnPheAla 40

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Db 89 GTT-----CTTGAGCATCAGGACCAACATCGCTGGCGAGTACCAGTCTTCACC 139
Qy 41 HisGlyAsnHisHisHisHisHisGlySerAlaAlaAspTyrProValProPro 60
Db 140 CAAGGC---CACACACACACACACACGCGCGCGCGGACTACCCACCGCCACCGCA 196
Qy 61 ProAsp---AsnPheAspHisArgArgThrTrpThrArgProPheHisGluThrAla 79
Db 197 CCGTCGGCCAAATTCGCCCACTGCAGATCATGGACACACACCGCTTCATGAACAGCAGCT 256
Qy 80 AlaGlyAsnSerSerArgLeuThrLeuGluValGlyAlaGlyGlnHisMetAlaHis 99
Db 257 GCAGGGAACAGCAGCAGCTACCGCTGGAGGTAGATGCAGGCGCCCAAAACATGGCTCAC 316
Qy 100 LeuValGlnProProAlaAlaHis-----IleValProPheTyrGlyGlyAlaPhe 117
Db 317 CTGCTGCAGCCACCGCCGACCAACACCATCGTCCCATTCCTGCGGGCTGCATTC 376
Qy 118 ThrAsnThrIleSerAsnGluAlaIleMetThrIleAspThrGluMetMetValGlyPro 137
Db 377 ACCAGCACTATTAGCAATCAACAATCATGACTATTATGATACAGATGATGGTGGGCT 436
Qy 138 AlaHisTyrProThrMetGlnGluArgAlaAlaLysValMetArgTyrArgGluLysArg 157
Db 437 GCCCATAACTGACGATGAGGAGAGAGAGGCGAAGGTGATGAGGTACAGGAGAGAGG 496
Qy 158 LysArgArgArgTyrAspLysGlnIleArgTyrGluSerArgLysAlaTyrAlaGluLeu 177
Db 497 AGAGCGGTGTATGACAGCAATCCGCTACGAGTCCAGAAAGCTTACCCGAGCTC 556
Qy 178 ArgProArgValAsnGlyArgPheValLys 187
Db 557 AGGCCAGCGGTCAATGGCTGCTTGTCAAG 586

RESULT 10
AY485976 712 bp mRNA linear PLN 17-MAR-2004
LOCUS Triticum monococcum cultivar Piz272561 ZCCT2 (VRN2) mRNA, complete
DEFINITION cds.
ACCESSION AY485976
VERSION AY485976.1 GI:45390733
KEYWORDS Triticum monococcum
SOURCE Triticum monococcum
ORGANISM Triticum monococcum

REFERENCE
AUTHORS Yan, L., Loukianov, A., Blechl, A., Tranquilli, G., Ramakrishna, W.,
SanMiguel, P., Bennett, J. L., Echenique, V. and Dubcovsky, J.
The Wheat VRN2 Gene Is a Flowering Repressor Down-Regulated by
Vernalization
JOURNAL Science 303 (5664), 1640-1644 (2004)
PUBMED 15016992
REFERENCE 2 (bases 1 to 712)
AUTHORS Yan, L., Loukianov, A., Blechl, A., Tranquilli, G., Ramakrishna, W.,
SanMiguel, P., Bennett, J. L., Echenique, V. and Dubcovsky, J.
Direct Submission
JOURNAL Submitted (20-NOV-2003) Agronomy and Range Science, University of
California, One Shields Avenue, Davis, CA 95616, USA
FEATURES
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domains"
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Alignment Scores:
Pred. No.: 2,148-45 Length: 712
Score: 730.50 Matches: 144
Percent Similarity: 81.6% Conservative: 11
Best Local Similarity: 75.8% Mismatches: 28
Query Match: 69.7% Indels: 7
DB: 15 Gaps: 4

US-10-723-947-77 (1-187) x AY485976 (1-712)
Qy 1 MetSerMetSerCysGlyLeuCysGlyAlaAsnAsnCysProArgLeuMetValSerPro 20
Db 29 ATGTCATGTCATCGGTTTGTGGCGCAAGCGACTGCCCGCACCATGATCTCGCC 88
Qy 21 IleHisHisHisHisHisHisGlnGlnHisGlnLeuCysGluTyrGlnPhePheAla 40
Db 89 GTT-----CTTGAGCATCAGGACCAACATCGCTGGCGAGTACCAGTCTTCACC 139
Qy 41 HisGlyAsnHisHisHisHisHisGlySerAlaAlaAspTyrProValProPro 60
Db 140 CAAGGC---CACACACACACACACGCGCGCGGACTACCCACCGCCACCGCA 196
Qy 61 ProAsp---AsnPheAspHisHisHisHisGlySerAlaAlaAspTyrProValPro 79
Db 197 CCGTCGGCCAAATTCGCCCACTGCAGATCATGGACACACACCGCTTCATGAACAGCAGCT 256
Qy 80 AlaGlyAsnSerSerArgLeuThrLeuGluValGlyAlaGlyGlnHisMetAlaHis 99
Db 257 GCAGGGAACAGCAGCAGCTACCGCTGGAGGTAGATGCAGGCGCCCAAAACATGGCTCAC 316
Qy 100 LeuValGlnProProAlaAlaHis-----IleValProPheTyrGlyGlyAlaPhe 117
Db 317 CTGCTGCAGCCACCGCCGACCAACACCATCGTCCCATTCCTGCGGGCTGCATTC 376
Qy 118 ThrAsnThrIleSerAsnGluAlaIleMetThrIleAspThrGluMetMetValGlyPro 137
Db 377 ACCAGCACTATTAGCAATCAACAATCATGACTATTATGATACAGATGATGGTGGGCT 436
Qy 138 AlaHisTyrProThrMetGlnGluArgAlaAlaLysValMetArgTyrArgGluLysArg 157
Db 437 GCCCATAACTGACGATGAGGAGAGAGAGGCGAAGGTGATGAGGTACAGGAGAGAGG 496
Qy 158 LysArgArgArgTyrAspLysGlnIleArgTyrGluSerArgLysAlaTyrAlaGluLeu 177
Db 497 AGAGCGGTGTATGACAGCAATCCGCTACGAGTCCAGAAAGCTTACCCGAGCTC 556
Qy 178 ArgProArgValAsnGlyArgPheValLys 187
Db 557 AGGCCAGCGGTCAATGGCTGCTTGTCAAG 586

RESULT 11
AY485979 2078 bp DNA linear PLN 17-MAR-2004
LOCUS Triticum turgidum cultivar Langdon ZCCT1-Td (VRN2) gene, complete
DEFINITION cds.
ACCESSION AY485979
VERSION AY485979.1 GI:45390744
KEYWORDS Triticum turgidum
SOURCE Triticum turgidum
ORGANISM Triticum turgidum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

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REFERENCE	Pooideae; Triticeae; Triticum.	QY	109	-----	109
AUTHORS	1 (bases 1 to 2078)	Db	435	TTGCCGATGGATGGCTCCCTGGCTTCCTTAAATAATCCCACTAATTTATGTCATC	494
TITLE	Yan,L., Loukianov,A., Blechl,A., Tranquilli,G., Ramakrishna,W., SanMiguel,P., Bennetzen,J.L., Echenique,V. and Dubcovsky,J. The wheat VRN2 Gene is a Flowering Repressor Down-Regulated by Vernalization	QY	109	-----	109
JOURNAL	Science 303 (5664), 1640-1644 (2004)	Db	495	TATACCCACTACAAAAAATAGCACCATGTAAACCATCTCATATATCTGTACATAATCTCT	554
REFERENCE	15016992	QY	109	-----	109
AUTHORS	2 (bases 1 to 2078)	Db	555	GTTAATGTACGCTGCTCAATTGTTCTCTGAAAAAGATATGCGGAATGGATCTTGTATAT	614
TITLE	SanMiguel,P., Bennetzen,J.L., Echenique,V. and Dubcovsky,J. Direct Submission	QY	109	-----	109
JOURNAL	Submitted (20-NOV-2003) Agronomy and Range Science, University of California, One Shields Avenue, Davis, CA 95616, USA	Db	615	TCTTTAATTTCTATGGAGGCATATATAGAGTTTGTGTTGTATAGTTGATGCGAAT	674
FEATURES	Location/Qualifiers	QY	109	-----	109
source	1. .2078	Db	675	TGTATGGTTGTCAAAATCATCAGTCATACATATAAACTTATTTTATTTTGGACCAAC	734
gene	/organism="Triticum turgidum"	QY	109	-----	109
mRNA	/mol_type="genomic DNA"	Db	735	AACAAAGTAATCAGTCATACATGATGATACTGAAAAATTTGACTTGTGTTCAATAA	794
CDS	/cultivar="Langdon"	QY	109	-----	109
	/db_xref="taxon:4571"	Db	795	ACTCGACCGCACAGCTGGGGGAAGACTTTAATCAAGCTGCTAGCTAGAGCTTAATAA	854
	/clone="BAC 354M17"	QY	109	-----	109
	/note="winter line; tetraploid genome A"	Db	855	TAAATATCTCTTTATGGATCAAGCAATACATATGCGCTCAATTTCTCAACTTGTCA	914
	<96. .>1965	QY	109	-----	109
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	join(<96. .401,1651. .>1965)	QY	109	-----	109
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	/product="ZCCT1-Td"	QY	109	-----	109
	/protein_id="AB560251.1"	Db	1155	AACTGATCGAGTCGGGTCCAAAAAAGAACAAACCCATACAAAAATGGAAGAGATC	1214
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	HHHVPVLPFPANFDSRTWTFPHETAAGNSSRLTLEVGAGRPMAHLVOPPARAH	QY	109	-----	109
	VFYFGAFTNTISNAITIDTEMVGPAPHTMQERAARKVMRYREKRRRRYDQIR	Db	1275	ATGGCATGTTCAACCCCAACCGGACTCAGATCAATATTATGTATGAAGTTACG	1334
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ORIGIN		Db	1335	AAACTCATAAACTGTATACATGTACAGGGCTACACATGTATACATATACACCTA	1394
Alignment Scores:		QY	109	-----	109
Pred. No.:	1.93e-40	Db	1395	TAAAAAGTATATTCTGTAGACCAATTTGTTTGGACGGTGCACATCTTTGAAAAA	1454
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Percent Similarity:	28.3%	Db	1455	AGAGGAGTTGTTAGCTTCCACTGTCCAGAAATAGTAATAGTTACAATCAAGTGC	1514
Best Local Similarity:	27.8%	QY	109	-----	109
Query Match:	64.0%	Db	109	-----	109
Indels:	424	QY	109	-----	109
Gaps:	2	Db	109	-----	109
US-10-723-947-77 (1-187) x AY485979 (1-2078)		QY	109	-----	109
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QY	101 ValGlnProProAlaArgAlaHisIle-----	Db	109	-----	109
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QY 164 sGlnIleArgTyrGluSerArgLysAlaTyrAlaGluLeuArgProArgValAsnGlyAr 184

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QY 184 gPheValLys 187

Db 1875 CTTTGTCAAG 1884

RESULT 12

LOCUS AY485977

DEFINITION Hordeum vulgare cultivar Dairiokaku ZCCT-Ha (VRN2) gene, partial cds.

ACCESSION AY485977

VERSION AY485977.1 GI:45390737

KEYWORDS

SOURCE Hordeum vulgare

ORGANISM Hordeum vulgare

REFERENCE 1 (bases 1 to 1985)

AUTHORS Yan, L., Loukolanov, A., Blechl, A., Tranquillini, G., Ramakrishna, W., SanMiguel, P., Bennett, J. L., Echenique, V. and Dubcovsky, J.

TITLE The Wheat VRN2 Gene Is a Flowering Repressor Down-Regulated by Vernalization

JOURNAL Science 303 (5664), 1640-1644 (2004)

PUBMED 15016992

REFERENCE 2 (bases 1 to 1985)

AUTHORS Yan, L., Loukolanov, A., Blechl, A., Tranquillini, G., Ramakrishna, W., SanMiguel, P., Bennett, J. L., Echenique, V. and Dubcovsky, J.

TITLE Direct Submission

JOURNAL Submitted (20-NOV-2003) Agronomy and Range Science, University of California, One Shields Avenue, Davis, CA 95616, USA

FEATURES

source

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Query Match: 56.3% Indels: 342

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QY 105 ----- 105

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QY 105 ----- 105

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LOCUS Hordeum vulgare cultivar Dairokkaku ZCCT-Hb (VRN2) gene, partial  
DEFINITION cds.  
ACCESSION AY485978  
VERSION AY485978.1 GI:45390740  
KEYWORDS  
SOURCE Hordeum vulgare  
ORGANISM Hordeum vulgare  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Poideae; Triticeae; Hordeum.  
REFERENCE 1 (bases 1 to 2064)  
Yan, L., Loukianov, A., Blechl, A., Tranquilli, G., Ramakrishna, W.,  
SanMiguel, P., Bennett, J. L., Echenique, V. and Dubcovsky, J.  
TITLE The Wheat VRN2 Gene Is a Flowering Repressor Down-Regulated by  
vernalization  
JOURNAL Science 303 (5664), 1640-1644 (2004)  
PUBMED 15016992  
REFERENCE 2 (bases 1 to 2064)  
Yan, L., Loukianov, A., Blechl, A., Tranquilli, G., Ramakrishna, W.,  
SanMiguel, P., Bennett, J. L., Echenique, V. and Dubcovsky, J.  
TITLE Direct Submission

JOURNAL Submitted (20-NOV-2003) Agronomy and Range Science, University of  
California, One Shields Avenue, Davis, CA 95616, USA  
FEATURES  
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Submitted (20-NOV-2003) Agronomy and Range Science, University of  
California, One Shields Avenue, Davis, CA 95616, USA  
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DEFINITION Triticum turgidum cultivar Langdon ZCCT2-Td (VRN2) gene, complete
cds.
ACCESSION AY485980
VERSION AY485980.1 GI:45390748
KEYWORDS Triticum turgidum
SOURCE Triticum turgidum
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Triticum.
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REFERENCE
AUTHORS
TITLE
JOURNAL
PUBMED
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
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1 (bases 1 to 1790)
Yan, L., Loukianov, A., Blechl, A., Tranquillini, G., Ramakrishna, W.,
SanMiguel, P., Bennetzen, J.L., Echenique, V. and Dubcovsky, J.
The wheat VRN2 gene is a flowering repressor down-regulated by
vernalization
Science 303 (5664), 1640-1644 (2004)
15016992
2 (bases 1 to 1790)
Yan, L., Loukianov, A., Blechl, A., Tranquillini, G., Ramakrishna, W.,
SanMiguel, P., Bennetzen, J.L., Echenique, V. and Dubcovsky, J.
Direct submission
Submitted (20-NOV-2003) Agronomy and Range Science, University of
California, One Shields Avenue, Davis, CA 95616, USA
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GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: February 23, 2006, 11:41:24 ; Search time 1488 Seconds  
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Total number of hits satisfying chosen parameters: 14418242

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Post-processing: Minimum Match 0%

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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10	124.5	11.9	114801	12	US-11-121-086-22	Sequence 22, Appl
11	124	11.8	1544	12	US-11-010-239-112	Sequence 112, App
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13	122	11.6	162013	12	US-11-150-888-30	Sequence 30, Appl
14	120	11.5	1864	6	US-09-925-065A-48799	Sequence 48799, A
15	120	11.5	1864	6	US-09-925-065A-48800	Sequence 48800, A
16	120	11.5	1864	6	US-09-925-065A-48801	Sequence 48801, A
17	120	11.5	1864	6	US-09-925-065A-48802	Sequence 48802, A
18	119.5	11.4	193321	12	US-11-121-086-10	Sequence 10, Appl
19	118	11.3	558	6	US-09-925-065A-438118	Sequence 438118, A
20	117	11.2	201	12	US-11-124-367A-26036	Sequence 26036, A
21	117	11.2	1088	6	US-09-925-065A-69151	Sequence 69151, A
22	117	11.2	70513	8	US-10-995-561-13368	Sequence 13368, A
23	116.5	11.1	628	6	US-09-925-065A-640012	Sequence 640012, A
24	116.5	11.1	93112	8	US-10-995-561-13234	Sequence 13234, A
25	116	11.1	201	12	US-11-124-367A-5731	Sequence 5731, Ap
26	115.5	11.0	959	6	US-09-925-065A-88250	Sequence 88250, A
27	115.5	11.0	959	6	US-09-925-065A-88251	Sequence 88251, A
28	114.5	10.9	615	6	US-09-925-065A-433631	Sequence 433631, A
29	114	10.9	658	6	US-09-925-065A-883427	Sequence 883427, A
30	114	10.9	3457	8	US-10-750-185-50627	Sequence 50627, A
31	114	10.9	3457	8	US-10-750-623-50627	Sequence 50627, A
32	113.5	10.8	577	6	US-09-925-065A-119552	Sequence 119552, A
33	113.5	10.8	772	6	US-09-925-065A-934808	Sequence 934808, A
34	113	10.8	1475	6	US-09-925-065A-688310	Sequence 688310, A
35	112.5	10.7	600	12	US-11-136-527-6342	Sequence 6342, Ap
36	112.5	10.7	1414	12	US-11-136-527-2246	Sequence 2246, Ap
37	112.5	10.7	158468	12	US-11-112-908-56	Sequence 56, Appl
38	112.5	10.7	193789	12	US-11-112-908-55	Sequence 55, Appl
39	112	10.7	554	6	US-09-925-065A-408177	Sequence 408177, A
40	112	10.7	6497	8	US-10-821-234-839	Sequence 839, App
41	111.5	10.6	463	6	US-09-925-065A-213874	Sequence 213874, A
42	111.5	10.6	1662	12	US-11-136-619-3	Sequence 3, Appli
43	111	10.6	1152	7	US-10-714-887-349	Sequence 349, App
44	111	10.6	1189	8	US-10-055-877-29	Sequence 29, Appl
45	111	10.6	2840	12	US-11-136-527-2131	Sequence 2131, Ap

#### ALIGNMENTS

RESULT 1  
US-11-121-086-62  
; Sequence 62, Application US/11121086  
; Publication No. US20050266459A1  
; GENERAL INFORMATION:  
; APPLICANT: POULSEN, TIM S.  
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES  
; FILE REFERENCE: 09138.6000-00000  
; CURRENT APPLICATION NUMBER: US/11/121,086  
; CURRENT FILING DATE: 2005-05-04  
; PRIOR APPLICATION NUMBER: 60/567,570  
; PRIOR FILING DATE: 2004-05-04  
; NUMBER OF SEQ ID NOS: 107  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 62  
; LENGTH: 200628  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-11-121-086-62

Alignment Scores:	1.57	Length:	200628
Pred. No.:	130.00	Matches:	21
Score:	57.8%	Conservative:	5
Best Local Similarity:	46.7%	Mismatches:	19
Query Match:	12.4%	Indels:	1
DB:	12	Gaps:	0



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2162	CATCACCACCACCATCACCACCACCAATCGTCACCACCGCGTGTGGCAAGCCA	2221

US-11-136-527-3235  
; Sequence 3235, Application US/11136527  
; Publication No. US20050287570A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Mounts, William M  
; TITLE OF INVENTION: Probe Arrays For



[illegible]



Db 104820 CATCACCATCACCACCACCATCACCA-TTATCATTACCACAACCATCATCACCACCA 104762

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; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 48800
; LENGTH: 1864
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-48800

Alignment Scores:
Pred. No.: 0.0948 Length: 1864
Score: 120.00 Matches: 25
Percent Similarity: 42.5% Conservative: 6
Best Local Similarity: 34.2% Mismatches: 24
Query Match: 11.5% Indels: 18
DB: 6 Gaps: 4

US-10-723-947-77 (1-187) x US-09-925-065A-48800 (1-1864)

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Db 1707 C A C A T C A C C G T C A T C A T C A T C A T C A T C A T C A T C A C A C A T T G C C A T C C T C A T T A C ----- 1654
                                     ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 42 G l y A s n H i s H i s H i s H i s G l y S e r A l a A l a A s p T y r P r o V a l P r o P r o P r o 61
Db 1653 C A C G A T C A T C A C C A C C A T C A T C A T G G C ----- C A T C A C C A C C A C C C T C C T C C T C C T 1603
                                     : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 62 A s p A s n P h e A s p H i s A r g A g T h r T p T h r A r g P r o P h e H i s G l u ----- 76
Db 1602 ----- C T T C A T C C T T C C T T C T C T C A T C A T C A C C A N A G T T G C C G 1564
                                     ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 77 --- T h r A l a A l a G l y A s n S e r S e r A r g L e u T h r L e u 88
Db 1563 T G C A C A C T T A G T A T C A T C A C A C A C A C A C T C T C T T A G T G T T G 1525
                                     ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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